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OM protein - protein search, using sw model

Run on: November 19, 2004, 13:48:23 ; Search time 156 Seconds
(without alignments)
427.716 Million cell updates/sec

Title: US-10-650-417-7
Perfect score: 978
Sequence: 1 VGLNLCIVAVSQNMIGIKNG.....SDVQEKGIKYKPEVVEKND 186

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	978	100.0	186	8	Adk19667 Human di
2	968	99.0	186	3	Aay63976 DHFR-HM p
3	968	99.0	187	4	Aam33902 Human pol
4	968	99.0	187	8	Adq09318 Human DHF
5	957.5	97.9	187	2	Raw81770 DHFR-HM p
6	880	90.0	186	6	AbR56964 Mouse di
7	880	90.0	186	7	AdA45852 Rat Prote
8	880	90.0	187	7	Raw37340 Mouse di
9	880	90.0	187	7	AdE60366 Rat Prote
10	878	89.8	187	8	Adk19665 Rat dihyd
11	875	89.5	187	8	Adn99572 Novel hum
12	875	89.5	187	8	Adn99573 Novel hum
13	874	89.4	186	1	Aap40064 Sequence
14	874	89.4	198	4	Aam41688 Human pol
15	874	89.4	204	2	AAR07470 Transcrip
16	874	89.4	209	2	AAR07471 Transcrip
17	874	89.4	266	1	AAP91236
18	874	89.4	524	2	AAR98136 (Hexahis)
19	874	89.4	539	2	AAR98137 DHFR/HPH
20	874	89.4	539	2	AAR98138 DHFR/HPH
21	869	88.9	186	2	AAR05742 376-8400
22	866	88.5	471	2	AAR27246 Sequence
23	864	88.3	193	2	AAR78376 Heat-indu
24	864	88.3	193	2	AAR99400 N-termina
25	864	88.3	297	4	Aab61618 MGP-DHFR

26	864	88.3	368	3	AAB12253
27	864	88.3	439	3	AAB12252
28	862	88.1	187	8	Adk19666
29	844.5	86.3	218	4	ABG16781 Novel hum
30	792.5	81.0	203	4	AAG10726 Novel hum
31	729	74.5	141	6	ABR56965 Human di
32	658	67.3	141	6	ABR56966 Mouse di
33	599.5	61.3	188	3	AAB53124 Macaca mu
34	587.5	60.1	188	8	Adk19664 Monkey di
35	553	56.5	141	6	ABR56967 Chicken d
36	472.5	48.3	210	2	AAW40101 Human her
37	472.5	48.3	210	2	AAW82437 KSHV DHFR
38	399	40.8	182	4	ABR69904 Drosophill
39	295.5	30.2	206	2	ABR69904
40	293.5	30.0	206	2	AAR28837 Pneumocys
41	284	29.0	612	2	AAU17271 N. caninu
42	239	24.4	168	4	AAU36186 Pseudomon
43	239	24.4	168	6	ABU38240 Protein e
44	239	24.4	168	8	AD025537 P_aerugin
45	239	24.4	168	8	AD025539 P_aerugin

ALIGNMENTS

RESULT 1
ADK19667
ID ADK19667 standard; protein; 186 AA.
XX ADK19667;
XX
XX 03-JUN-2004 (first entry)
XX Human dihydrofolate reductase (DHFR) polypeptide.
XX
XX Human; dihydrofolate reductase; DHFR; methotrexate; herpes simplex virus;
KW thymidine kinase; cytosine deaminase; pro-apoptotic gene;
KW immunostimulatory molecule; tumour suppressor gene; beta-globin protein;
KW green fluorescent protein; cancer; colorectal; liver; pancreas; lymphoma;
KW lung; prostate; breast; suicide gene; cytostatic; enzyme.
XX Homo sapiens.
XX US2004053836-A1.
XX
XX 18-MAR-2004.
XX
XX 22-APR-2003; 2003US-00421285.
XX
XX 22-APR-2003; 2002US-0375250P.
XX
XX (MAYE/) MAYER-KUCKUK P.
XX (BANE/) BANERJEE D.
XX (BERT/) BERTINO J.
XX
XX Mayer-Kuckuk P, Banerjee D, Bertino J;
XX WPI; 2004-247775/23.
XX
XX Novel cDNA molecule encoding fusion protein that comprises mammalian
PT dihydrofolate reductase and a therapeutic protein such as product of
PT tumor suppressor gene, useful for treating colorectal cancer, liver
PT cancer, pancreatic cancer.
XX
XX Disclosure; SEQ ID NO 5; 27pp; English.
XX
XX The invention relates to a cDNA molecule encoding a fusion protein that
CC comprises a mammalian dihydrofolate reductase (DHFR) and a therapeutic
CC protein. The fusion protein comprises a wild-type mammalian DHFR such as
CC rat, mouse, dog, monkey or human DHFR. Optionally, the fusion protein
CC comprises a mutant form of DHFR, preferably a mutant form of human DHFR,
CC where the mutant form has increased resistance to methotrexate. The cDNA
CC molecule is useful for providing enhanced delivery of a therapeutic

CC Protein to a mammalian subject which involves administering the cDNA. The
 CC therapeutic protein is a protein that enhances toxicity of an
 CC administered drug such as a mutant or wild-type form of herpes simplex
 CC virus thymidine kinase or cytosine deaminase. The therapeutic protein is
 CC a product of a pro-apoptotic gene, an immunostimulatory molecule, a
 CC product of a tumour suppressor gene or a functional protein useful in
 CC gene therapy such as a wild-type or enhanced beta-globin protein. The
 CC cDNA further comprises a region encoding a reporter protein such as green
 CC fluorescent protein. The cDNA molecules can be used for treating a wide
 CC variety of cancer cells e.g., colorectal cancer, liver cancer, pancreatic
 CC cancer, lymphomas, lung cancer, prostate cancer and breast cancer using
 CC suicide genes as therapeutic genes. This sequence represents a human DHFR
 CC polypeptide of the invention.

XX Sequence 186 AA;
 SQ Query Match 100.0%; Score 978; DB 8; Length 186;
 Best Local Similarity 100.0%; Pred. No. 8.8e-99;
 Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VGSNCIVAVSQNMIGKNGDLPWFLNEFRYFORMTTSSVEGKQNLVIMGKKTWFSI 60
 DB 1 VGSNCIVAVSQNMIGKNGDLPWFLNEFRYFORMTTSSVEGKQNLVIMGKKTWFSI 60
 QY 61 PEKRPKGRINLVLSRELKPPQCAHFLSRSLDDALKLTPQPELANKVDVWVVGSSV 120
 DB 61 PEKRPKGRINLVLSRELKPPQCAHFLSRSLDDALKLTPQPELANKVDVWVVGSSV 120
 QY 121 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYLLPEYPGVLSVQBEKGKIKYKFE 180
 DB 121 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYLLPEYPGVLSVQBEKGKIKYKFE 180
 QY 181 VYEKND 186
 DB 181 VYEKND 186

RESULT 2
 AAM39976
 ID AAM39976 standard; protein; 186 AA.
 XX AAY69976;
 AC AAY69976;
 DT 13-APR-2000 (first entry)
 DE DHFR-HM protein.
 KW Protein sequence database; biological function determination;
 KW enzymatic activity; signaling activity; protein function determination;
 KW DHFR-HM.
 XX Homo sapiens.
 PN WO9962004-A1.
 XX WO9962004-A1.
 DE 02-DEC-1999.
 PF 26-MAY-1998; 98WO-JP002302.
 PR 26-MAY-1998; 98WO-JP002302.
 XX (MEDI-) INST MEDICINAL MOLECULAR DESIGN INC.
 XX Itai A, Tomioka N, Itai R, Imamura M;
 XX WPI; 2000-136797/12.
 XX An efficient, accurate and rapid computer database for estimating protein
 XX functions e.g. enzymatic activity, for polypeptides obtained from gene
 XX sequence translation.
 XX Example 2; Fig 2; 26pp; Japanese.
 XX

CC This sequence represents the human DHFR protein. The invention relates to
 CC a database containing information on the amino acid (aa) sequences of
 CC proteins of which 1 or more biological functions are known. The database
 CC also contains additional information on the score of importance of each
 CC aa residue in the whole aa sequence in determining the known biological
 CC functions. The invention also relates to a method of preparing an
 CC alignment between aa sequences contained in the database and those of the
 CC unknown polypeptide. This is represented as the homology amongst various
 CC sites, each being identified as having a high score of importance in
 CC determining potential biological functions. The method is used to enable
 CC an efficient estimation of the biological functions (particularly
 CC enzymatic and signaling activities) of polypeptides from their aa
 CC sequences. Suitable proteins can then be isolated and purified by various
 CC means. This could be of considerable use in a biological and medical
 CC context. The computerised procedure is efficient, fast and accurate
 XX

SQ Sequence 186 AA;
 Query Match 99.0%; Score 968; DB 3; Length 186;
 Best Local Similarity 99.5%; Pred. No. 1.1e-97;
 Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VGSNCIVAVSQNMIGKNGDLPWFLNEFRYFORMTTSSVEGKQNLVIMGKKTWFSI 60
 DB 1 VGSNCIVAVSQNMIGKNGDLPWFLNEFRYFORMTTSSVEGKQNLVIMGKKTWFSI 60
 QY 61 PEKRPKGRINLVLSRELKPPQCAHFLSRSLDDALKLTPQPELANKVDVWVVGSSV 120
 DB 61 PEKRPKGRINLVLSRELKPPQCAHFLSRSLDDALKLTPQPELANKVDVWVVGSSV 120
 QY 121 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYLLPEYPGVLSVQBEKGKIKYKFE 180
 DB 121 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYLLPEYPGVLSVQBEKGKIKYKFE 180
 QY 181 VYEKND 186
 DB 181 VYEKND 186

RESULT 3
 AAM39902
 ID AAM39902 standard; protein; 187 AA.
 XX AAM39902;
 AC AAM39902;
 DT 22-OCT-2001 (first entry)
 DE Human polypeptide SEQ ID NO 3047.
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX Homo sapiens.
 OS WO200153312-A1.
 PN 26-JUL-2001.
 PD 26-DEC-2000; 2000WO-US034263.
 XX 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00623312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

XX PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;

XX PI Zhou P, Goodrich R, Dimañac RT;

XX DR WPI; 2001-442253/47.

XX DR N-PSDB; AAI59058.

XX PT Novel nucleic acids and polypeptides, useful for treating disorders such

XX PT as central nervous system injuries.

XX PS Example 4; SEQ ID NO 3047; 10078pp; English.

XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the

XX CC encoded polypeptides (AAI38642-AAI42213) with nootropic,

XX CC immunosuppressant and cytostatic activity. The polynucleotides are useful

XX CC in gene therapy. A composition containing a polypeptide or polynucleotide

XX CC of the invention may be used to treat diseases of the peripheral nervous

XX CC system, such as peripheral nervous injuries, peripheral neuropathy and

XX CC localised neuropathies and central nervous system diseases, such as

XX CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

XX CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

XX CC utilisation of the activities such as: Immune system suppression,

XX CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

XX CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,

XX CC assays for receptor activity, arthritis and inflammation, leukaemias and

XX CC C.N.S disorders. Note: The sequence data for this patent did not form

XX CC part of the printed specification

XX SQ Sequence 187 AA;

Query Match 99.0%; Score 968; DB 4; Length 187;

Best Local Similarity 99.5%; Pred. No. 1.1e-97;

Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VGSNCIVAVSQNGIGKNGDLPPELNEFRYFORWTTSSVEGKNLVIMGKKTWFSI 60

Db 2 VGSNCIVAVSQNGIGKNGDLPPELNEFRYFORWTTSSVEGKNLVIMGKKTWFSI 61

Qy 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDWVIVGSSV 120

Db 62 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDWVIVGSSV 121

Qy 121 YKEAMNHGHLKLPVTRIMQDFSDTFPPIDLEKYLLPEYGVLSDVQEEKIKYKFE 180

Db 122 YKEAMNHGHLKLPVTRIMQDFSDTFPPIDLEKYLLPEYGVLSDVQEEKIKYKFE 181

Qy 181 VYEKND 186

Db 182 VYEKND 187

RESULT 4

ADQ09318

ID ADQ09318 standard; protein; 187 AA.

XX AC ADQ09318;

XX DT 23-SEP-2004 (first entry)

XX DE Human DHFR protein SEQ ID NO:503.

XX KW thanatosis-associated protein; THAP; THAP responsive gene; THAP family;

XX KW THAP responsive element; angiogenesis; inflammation; metastasis; cancer;

XX KW apoptosis; cardiovascular disease; neurodegenerative disease; chemokine;

XX KW antiangiogenic; antiinflammatory; cardiovascular; cytostatic;

XX KW neuroprotective; osteopathic; THAP modulator; THAP synthesis modulator;

XX KW human.

XX OS Homo sapiens.

XX

Query Match 99.0%; Score 968; DB 8; Length 187;

Best Local Similarity 99.5%; Pred. No. 1.1e-97;

Sequence 187 AA;

PN WO2004055050-A2.

XX PD 01-JUL-2004.

XX PF 10-DEC-2003; 2003WO-IB006434.

XX PR 10-DEC-2002; 2002US-0432699P.

XX PR 03-JUL-2003; 2003US-0485027P.

XX XX (ENDO-) ENDOCUBE SAS.

XX PA (CNRS) CNRS CENT NAT RECH SCI.

XX PI Girard J, Amalric F, Roussigne M, Clouaire T;

XX PI WPI; 2004-525034/50.

XX DR N-PSDB; ADQ09319.

XX CC Modulating expression of a Thanatos (death)-Associated Protein (THAP)

XX CC responsive gene for preventing or treating e.g. cancer or inflammation,

XX CC comprises modulating the interaction of a THAP polypeptide with a nucleic

XX CC acid.

XX CC Example 47; SEQ ID NO 503; 612pp; English.

XX CC The present invention describes a method for modulating the expression of

XX CC a thanatos (death)-associated protein (THAP) responsive gene. The method

XX CC comprises modulating the interaction of a THAP-family polypeptide or its

XX CC biological fragment with a nucleic acid, and so enhancing or repressing

XX CC the expression of the THAP responsive gene. Also described: (1) a method

XX CC of modulating the expression of a gene responsive to a THAP/chemokine

XX CC complex; (2) a pharmaceutical composition comprising a THAP-responsive

XX CC element in a pharmaceutical carrier; (3) a transcription factor decoy

XX CC consisting essentially of a THAP responsive element; (4) a cell

XX CC comprising a transcription factor decoy described above; (5) methods of

XX CC modulating the interaction between a nucleic acid and a THAP-family

XX CC polypeptide or its biological fragment, or a nucleic acid and a

XX CC THAP/chemokine complex; (6) a vector packaging cell line comprising a

XX CC cell comprising a viral vector which comprises a promoter operably linked

XX CC to a nucleic acid encoding a THAP-family polypeptide or its biological

XX CC fragment; (7) a method of constructing a cell which expresses a

XX CC recombinant THAP-family polypeptide; (8) a method of ameliorating

XX CC symptoms associated with a condition mediated by a THAP/chemokine complex

XX CC ; (9) methods of identifying a test compound that modulates transcription

XX CC at a THAP responsive element or that modulates the transport of a

XX CC chemokine into the nucleus; (10) methods for reducing the symptoms

XX CC associated with a condition selected from excessive or insufficient

XX CC angiogenesis, inflammation, metastasis of a cancerous tissue, excessive

XX CC or insufficient apoptosis, cardiovascular disease and neurodegenerative

XX CC diseases; symptoms associated with a condition resulting from the

XX CC activity of a chemokine or a THAP-family polypeptide in an individual; or

XX CC symptoms associated with transcriptional repression or activation

XX CC mediated by a THAP-family polypeptide in an individual; (11) a vector

XX CC comprising a THAP responsive promoter operably linked to a nucleic acid

XX CC encoding a detectable product; (12) a genetically engineered cell

XX CC comprising the vector described above or that expresses a THAP-family

XX CC polypeptide or its biological fragment; (13) an in vitro transcription

XX CC reaction comprising a nucleic acid comprising a THAP responsive promoter,

XX CC ribonucleotides and an RNA polymerase; and (14) an isolated mutant THAP-

XX CC family polypeptide that does not bind to a chemokine. The pharmaceutical

XX CC composition has antiangiogenic, antiinflammatory, cardiovascular,

XX CC cytosolic, neuroprotective and osteopathic activities, and can be used

XX CC as a THAP and THAP synthesis modulator. The composition can be used for

XX CC modulating the expression of a THAP responsive gene. Modulation is useful

XX CC for reducing symptoms of conditions such as excessive or insufficient

XX CC angiogenesis, inflammation, metastasis of a cancerous tissue, excessive

XX CC or insufficient apoptosis, cardiovascular disease or neurodegenerative

XX CC diseases. The present sequence is used in the exemplification of the

XX CC present invention.

XX SQ

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Matches 185: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
01 VGSNCIVAVSQNGIGKGGDLFWPEPLRNEFRYFQMTTTSVEGKQNLVIMGKKTWFSI 60
02 VGSNCIVAVSQNGIGKGGDLFWPEPLRNEFRYFQMTTTSVEGKQNLVIMGKKTWFSI 61
03
04 PEKNRPLKGRINVLVLSRELKEPPQGAHFLSRSLDALKLTQPELANKNVDMWTIVGSSV 120
05
06 PEKNRPLKGRINVLVLSRELKEPPQGAHFLSRSLDALKLTQPELANKNVDMWTIVGSSV 121
07
08 YKAMNHPGHLKFVTRIMQDPESDTFFPEIDLEKYKLLPEYPGVLSDVQEEKIGIKYKFE 180
09
10 YKAMNHPGHLKFVTRIMQDPESDTFFPEIDLEKYKLLPEYPGVLSDVQEEKIGIKYKFE 181
11
12 VYEKND 186
13
14 VYEKND 187
15
16

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RESULT 6
ABR56964
ID ABR56964 standard; protein; 186 AA.
XX
XX ABR56964;
XX AC
XX DT
XX DT (first entry)
XX 04-AUG-2003
XX Mouse dihydrofolate reductase amino acid sequence #1.
XX DE
XX XX
XX XX Dihydrofolate reductase; DYS; enzyme; browser; genetic; gene; database.
XX KW
XX OS
XX Mus musculus.
XX PN
XX WO2003017138-A1.
XX PD
XX 27-FEB-2003.
XX PF
XX 20-AUG-2002; 2002WO-JP008368.
XX PR
XX 21-AUG-2001; 2001US-0313488P.
XX {MEDI-} INST MEDICINAL MOLECULAR DESIGN INC.
XX PA
XX Fukuda M, Shigetaka M, Tomioka N, Itai A;
XX PI
XX WPI; 2003-268379/26.
XX DR
XX Method of browsing genetic sequences comprises specifying sequences,
XX PT determining similarity against database records, and displaying similar
XX PT sequences from database together with specified sequences.
XX PT
XX Example 1; Fig 2; 39pp; Japanese.
XX PS

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100 Sequence 187 Al;
Query Match          97.9%; Score 957.5; DB 2; Length 187;
Best local similarity 98.9%; Pred. NO. 1.6e-96;
Matches 185; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
1 VGS LNC I C V A V S Q N M G I G K G D L P W P L F L R N E P R Y F Q R M T T T S S V E G K O N L V I M G K T W F S I 60
1 VGS LNC I C V A V S Q N M G I G K G D L P W P L F L R N E P R Y F Q R M T T T S S V E G K O N L V I M G K T W F S I 60

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QY 121 YKAMNHPGHLKLVTRINQDPESTFFPEIDLEKYKLLPEYPGVLSDVQBEKGIKYFE 180
Db 121 YQAMNQPGLRLFVTRINQDPESTFFPEIDLGKYLPEYPGVLSEVQBEKGIKYFE 180
QY 181 VYEKND 186
Db 181 VYEKND 186

RESULT 7

ADD45852
ID ADD45852 standard; protein; 186 AA.

XX AC ADD45852;

XX DT 29-JAN-2004 (first entry)

XX DE Rat Protein P00375, SEQ ID NO 11522.

XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GHEO) GEN HOSPITAL CORP.

XX PA (FARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX DR WPI; 2003-268312/26.

XX DR GENBANK; P00375.

XX PT New composition comprising two or more isolated polypeptides, useful for
XX PT preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
XX CC derivative or allelic variation of the nucleic acid sequence. Also
XX CC claimed are a vector comprising the novel polynucleotide, a host cell
XX CC comprising the vector, a method for identifying a nucleotide sequence
XX CC which is differentially regulated in an animal subjected to pain and a
XX CC kit to perform the method, an array, a method for identifying an agent
XX CC that increases or decreases the expression of the polynucleotide sequence
XX CC that is differentially expressed in neuronal tissue of a first animal
XX CC subjected to pain, a method for identifying a compound which regulates
XX CC the expression of a polynucleotide sequence which is differentially
XX CC expressed in an animal subjected to pain, a method for identifying a
XX CC compound that regulates the activity of one or more of the
XX CC polynucleotides, a method for producing a pharmaceutical composition, a
XX CC method for identifying a compound or small molecule that regulates the
XX CC activity in an animal of one or more of the polypeptides given in the
XX CC specification, a method for identifying a compound useful in treating
XX CC pain and a pharmaceutical composition comprising the one or more
XX CC polypeptides or their antibodies. The polynucleotide or the compound that
XX CC modulates its activity is useful for preparing a medicament for treating
XX CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX CC therapy). The sequence presented is a rat protein (shown in Table 2 of
XX CC the specification) which is differentially expressed during pain. Note:
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic form directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 186 AA;

Query Match 90.0%; Score 880; DB 7; Length 186;
Best Local Similarity 89.2%; Pred. No. 5.1e-88;
Matches 166; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 VGSINCIVAVSQNGIGKNGDLPPFLRNEFRYFORMTTSSVEGKONLVIMGKKTWFSI 60
Db 1 VRFNCIVAVSQNGIGKNGDLPPFLRNEFRYFORMTTSSVEGKONLVIMGKKTWFSI 60

QY 61 PEKORPLKGRINLVLSRELKEPPQGAHFLSRSDLDALKLTEOPELANKYDMVWIVGSSV 120

Db 61 PEKORPLKGRINLVLSRELKEPPQGAHFLAKSLDDALRLIEQPELASKYDMVWIVGSSV 120

QY 121 YKAMNHPGHLKLVTRINQDPESTFFPEIDLEKYKLLPEYPGVLSDVQBEKGIKYFE 180

Db 121 YQAMNQPGLRLFVTRINQDPESTFFPEIDLGKYLPEYPGVLSEVQBEKGIKYFE 180

QY 181 VYEKND 186

Db 181 VYEKND 186

RESULT 8

AAW37340

ID AAW37340 standard; protein; 187 AA.

XX AC AAW37340;

XX DT 11-MAY-1998 (first entry)

XX DE Mouse dihydrofolate reductase.

XX KW Vaccine; B-cell malignancy; lymphoma; leukaemia; tumour;
XX KW gene amplification; immunotherapy; therapy; mouse; DHFR;
XX KW dihydrofolate reductase; vector; PSSD7-DHFR.

XX CS Mus musculus.

XX PN WO9741244-A1.

XX PD 06-NOV-1997.

XX PF 25-APR-1997; 97WO-US007039.

XX PR 01-MAY-1996; 96US-00644664.

XX PR 06-DEC-1996; 96US-00761277.

XX PA (GENI-) GENITOPE CORP.

XX PI Denney DW;

XX WPI; 1997-549743/50.

XX N-PSDB; AAT97170.

XX PT Multivalent vaccine to treat B cell lymphoma or leukaemia - comprises at
XX PT least 2 different recombinant variable regions of immunoglobulin
XX PT molecules derived from B cell lymphoma cells.

XX PS Example 3; Page 111; 177pp; English.

XX CC This protein comprises mouse dihydrofolate reductase (DHFR). The DHFR
XX CC coding sequence (see AAT97170) was utilised in the construction of
XX CC amplification vector PSSD75-DHFR, which contains the DHFR cDNA under
XX CC control of the SV40 enhancer/promoter. The vector allows the selection of
XX CC cell lines which have amplified the vector sequences by selecting for
XX CC cells able to grow in increasing concentrations of methotrexate. The
XX CC invention provides vectors and improved methods for the expression and co
XX CC -amplification of genes encoding recombinant proteins in cultured cells.
XX CC The methods permit the isolation of cell lines which have co-amplified
XX CC input recombinant sequences which encode an amplifiable marker, one or

CC more expression vectors encoding a protein of interest and optionally a
CC selectable marker. The amplified cells provide large quantities of
CC recombinant proteins suitable for immunotherapy for treatment of
CC lymphomas and leukaemias. The methods permit the production of custom
CC vaccines, including multivalent vaccines, that reflect the degree of
CC somatic variation found in a patient's tumour
XX

Sequence 187 AA;
Query Match 90.0%; Score 880; DB 2; Length 187;
Best Local Similarity 89.2%; Pred. No. 5.2e-88;
Matches 166; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
QY 1 VGSNCIVAVSQNMIGKNGDLPPFLNEFRYFQMTTSSVSGKQNLVIMGKKTWFSI 60
DB 2 VRPLNCIVAVSQNMIGKNGDLPPFLNEFRYFQMTTSSVSGKQNLVIMGKKTWFSI 61
QY 61 PEKNRPLKGRINVLVSRELKPPQGAHFLSRSLDDALKLIEOPELANKVDMWIVGGSSV 120
DB 62 PEKNRPLKGRINVLVSRELKPPQGAHFLSRSLDDALKLIEOPELANKVDMWIVGGSSV 121
QY 121 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSVQVEEKGIKYKFE 180
DB 122 YQEMNQPGHLRLFVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSVQVEEKGIKYKFE 181
QY 181 VYEKND 186
DB 182 VYEKND 187

RESULT 9
ADK19665
ID ADE60366 standard; protein; 187 AA.
AC ADE60366;
XX
XX
DE 29-JAN-2004 (first entry)
DE Rat Protein AAH05796, SEQ ID NO 6273.
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX Rattus norvegicus.
XX
XX WO2003016475-A2.
PD 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX
XX {GEHO } GEN HOSPITAL CORP.
XX {FARB } BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
XX GENBANK; AAH05796.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX

CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC the sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 187 AA;

Query Match 90.0%; Score 880; DB 7; Length 187;
Best Local Similarity 89.2%; Pred. No. 5.2e-88;
Matches 166; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
QY 1 VGSNCIVAVSQNMIGKNGDLPPFLNEFRYFQMTTSSVSGKQNLVIMGKKTWFSI 60
DB 2 VRPLNCIVAVSQNMIGKNGDLPPFLNEFRYFQMTTSSVSGKQNLVIMGKKTWFSI 61
QY 61 PEKNRPLKGRINVLVSRELKPPQGAHFLSRSLDDALKLIEOPELANKVDMWIVGGSSV 120
DB 62 PEKNRPLKGRINVLVSRELKPPQGAHFLSRSLDDALKLIEOPELANKVDMWIVGGSSV 121
QY 121 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSVQVEEKGIKYKFE 180
DB 122 YQEMNQPGHLRLFVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSVQVEEKGIKYKFE 181
QY 181 VYEKND 186
DB 182 VYEKND 187

RESULT 10
ADK19665
ID ADK19665 standard; protein; 187 AA.
AC ADK19665;
XX
XX
XX 03-JUN-2004 (first entry)
DE Rat dihydrofolate reductase (DHFR) polypeptide.
XX
XX Rat; dihydrofolate reductase; DHFR; methotrexate; herpes simplex virus;
KW thymidine kinase; cytosine deaminase; pro-apoptotic gene;
KW immunostimulatory molecule; tumour suppressor gene; beta-globin protein;
KW green fluorescent protein; cancer; colorectal; liver; pancreas;
KW lung; prostate; breast; suicide gene; cytostatic; enzyme.
XX
XX Rattus sp.
XX
XX US2004053836-A1.
XX
XX 18-MAR-2004.
XX
XX 22-APR-2003; 2003US-00421285.
XX
XX 22-APR-2002; 2002US-0375250P.
XX
XX (MAYE/) MAYER-KUCKUK P.
XX

PA (BANE//) BANERJEE D.
 PA (BERT//) BERTINO J.
 XX
 XX
 PI Mayer-Kucuk P, Banerjee D, Bertino J;
 XX
 XX WPI; 2004-247775/23.
 DR
 XX
 XX
 PT Novel cdna molecule encoding fusion protein that comprises mammalian
 PT dihydrofolate reductase and a therapeutic protein such as product of
 PT tumor suppressor gene, useful for treating colorectal cancer, liver
 PT cancer, pancreatic cancer.
 XX
 PS Disclosure; SEQ ID NO 3; 27pp; English.
 XX
 CC The invention relates to a cdna molecule encoding a fusion protein that
 CC comprises a mammalian dihydrofolate reductase (DHFR) and a therapeutic
 CC protein. The fusion protein comprises a wild-type mammalian DHFR such as
 CC rat, mouse, dog, monkey or human DHFR. Optionally, the fusion protein
 CC comprises a mutant form of DHFR, preferably a mutant form of human DHFR,
 CC where the mutant form has increased resistance to methotrexate. The cdna
 CC molecule is useful for providing enhanced delivery of a therapeutic
 CC protein to a mammalian subject which involves administering the cdna. The
 CC therapeutic protein is a protein that enhances toxicity of an
 CC administered drug such as a mutant or wild-type form of herpes simplex
 CC virus thymidine kinase or cytosine deaminase. The therapeutic protein is
 CC a product of a pro-apoptotic gene, an immunostimulatory molecule, a
 CC product of a tumor suppressor gene or a functional protein useful in
 CC gene therapy such as a wild-type or enhanced beta-globin protein. The
 CC cdna further comprises a region encoding a reporter protein such as green
 CC fluorescent protein. The cdna molecules can be used for treating a wide
 CC variety of cancer cells e.g., colorectal cancer, liver cancer, pancreatic
 CC cancer, lymphomas, lung cancer, prostate cancer and breast cancer using
 CC suicide genes as therapeutic genes. This sequence represents a rat DHFR
 CC polypeptide of the invention.
 XX
 SQ Sequence 187 AA;
 Query Match 89.8%; Score 878; DB 8; Length 187;
 Best Local Similarity 88.7%; Pred. No. 8.6e-88;
 Matches 165; Conservative 12; Mismatches 9; Indels 0; Gaps 0;
 Qy 1 VGLNCIVAVSQNNGIGKNGDLPWPLRNBFYQFMTTSSVEGKQNLVIMGKTKWFSI 60
 Db 2 VRPLNCIVAVSQNNGIGKNGDLPWPLRNBFYQFMTTSSVEGKQNLVIMGKTKWFSI 61
 Qy 61 PEKRPILKGRINVLSELKEPPGCAHFLSRSLDDALKLLEQPELANKVDVWVVGSSV 120
 Db 62 PEKRPILKDRINI VLSRELKEPPGCAHFLSRSLDDALKLLEQPELANKVDVWVVGSSV 121
 Qy 121 YKEAMNHGHLKLVTRIMODFESDTFFPEIDLEKYLPEYGVLSDVQEEKGIKYKFE 180
 Db 122 YQEAANQFGHLRLEVTIMQEFESDTFFPEIDLEKYLPEYGVLSDVQEEKGIKYKFE 181
 Qy 181 VYEKND 186
 Db 182 VYEKND 187
 RESULT 11
 ID ADN99572 standard; protein; 187 AA.
 XX
 AC ADN99572;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Novel human protein sequence #389.
 XX
 KW anti-inflammatory; dermatological; neuroprotective; immunomodulator;
 KW antibacterial; virucide; antipsoriatic; cytostatic; gene therapy;
 KW vaccine; inflammatory; CNS; immune disorder; cancer; psoriasis; diabetes;
 KW early aging; hormonal imbalance; ischemic heart disease;
 KW ulcerative colitis.
 XX

XX Homo sapiens.
 OS WO2004038003-A2.
 XX
 XX PD 06-MAY-2004.
 XX
 XX 24-OCT-2003; 2003WO-US033947.
 PF 25-OCT-2002; 2002US-0421061P.
 XX 25-OCT-2002; 2002US-0421080P.
 XX 25-OCT-2002; 2002US-0421552P.
 XX 25-OCT-2002; 2002US-0421614P.
 XX 30-OCT-2002; 2002US-0422177P.
 XX 30-OCT-2002; 2002US-0422178P.
 XX 15-NOV-2002; 2002US-042355P.
 XX 15-NOV-2002; 2002US-0423584P.
 XX 15-NOV-2002; 2002US-042394P.
 XX 15-NOV-2002; 2002US-042430P.
 XX 15-NOV-2002; 2002US-0426916P.
 XX 27-NOV-2002; 2002US-0429224P.
 XX 27-NOV-2002; 2002US-0429275P.
 XX 27-NOV-2002; 2002US-0429302P.
 XX 27-NOV-2002; 2002US-0429326P.
 XX 27-NOV-2002; 2002US-0429551P.
 XX 04-DEC-2002; 2002US-0430645P.
 XX 04-DEC-2002; 2002US-0430651P.
 XX 04-DEC-2002; 2002US-0430657P.
 XX 04-DEC-2002; 2002US-0430663P.
 XX 04-DEC-2002; 2002US-0430668P.
 XX 04-DEC-2002; 2002US-0430684P.
 XX 05-DEC-2002; 2002US-0430937P.
 XX 05-DEC-2002; 2002US-0430965P.
 XX 12-DEC-2002; 2002US-0431458P.
 XX 12-DEC-2002; 2002US-043251P.
 XX 13-DEC-2002; 2002US-0433500P.
 XX 13-DEC-2002; 2002US-0433318P.
 XX 23-DEC-2002; 2002US-0436236P.
 XX 03-JAN-2003; 2003US-0437914P.
 XX 17-JAN-2003; 2003US-0440820P.
 XX 18-APR-2003; 2003US-0463700P.
 XX 18-APR-2003; 2003US-0463708P.
 XX 18-APR-2003; 2003US-0463718P.
 XX 18-APR-2003; 2003US-0463732P.
 XX 02-MAY-2003; 2003US-0467199P.
 XX 02-MAY-2003; 2003US-0467201P.
 XX 02-MAY-2003; 2003US-0467203P.
 XX 02-MAY-2003; 2003US-0467230P.
 XX 19-MAY-2003; 2003US-0471308P.
 XX 19-MAY-2003; 2003US-0471336P.
 XX 22-MAY-2003; 2003US-0472420P.
 XX 09-JUN-2003; 2003US-0476609P.
 XX 09-JUN-2003; 2003US-0476621P.
 XX 09-JUN-2003; 2003US-0476632P.
 XX 09-JUN-2003; 2003US-0476641P.
 XX 08-JUL-2003; 2003US-0485217P.
 XX 08-JUL-2003; 2003US-0485218P.
 XX 08-JUL-2003; 2003US-0485223P.
 XX 08-JUL-2003; 2003US-0485224P.
 XX 08-JUL-2003; 2003US-0485325P.
 XX 08-JUL-2003; 2003US-0485359P.
 XX 14-JUL-2003; 2003US-0485446P.
 XX 14-JUL-2003; 2003US-0485480P.
 XX 15-JUL-2003; 2003US-0486891P.
 XX 15-JUL-2003; 2003US-0486960P.
 XX 08-AUG-2003; 2003US-0493341P.
 XX 08-AUG-2003; 2003US-0493370P.
 XX 08-AUG-2003; 2003US-0493573P.
 XX 08-AUG-2003; 2003US-0493577P.
 XX

PA (FIVE-) FIVE PRIME THERAPEUTICS INC.

XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
 PI Halenbeck RF, Kothakota S, Lin H, Linnemann T, Pierce K, Wang Y;
 PI Wong JGP, Wu G, Zhang H, Zeng C;
 XX
 DR WPI: 2004-365511/34.
 DR N-PSDB; ADN98789.

XX New nucleic acid molecules, useful in preparing a composition for
 PT treating or preventing e.g. inflammatory, CNS, bacterial or viral
 PT disorders, cancer, psoriasis, diabetes, ischemic heart disease or
 PT ulcerative colitis.

XX Claim 14; SEQ ID NO 1172; 532pp; English.

XX The invention relates to a nucleic acid molecule comprising a
 CC polynucleotide sequence or its complement that encodes a polypeptide. The
 CC nucleic acid is useful in preparing a composition for treating or
 CC preventing inflammatory, CNS, immune, bacterial or viral disorder.
 CC cancer, psoriasis, diabetes, early aging, hormonal imbalance, ischemic
 CC heart disease or ulcerative colitis. This sequence corresponds to a
 CC protein of the invention.

XX Sequence 187 AA;

Query Match 89.5%; Score 875; DB 8; Length 187;
 Best Local Similarity 92.9%; Pred. No. 1.8e-87;
 Matches 170; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
 4 LNCIVAVSQMGIKNGKNDLPWPLNRPYRFRMTTSSVEGKQNLVINGKKTWFSIPEX 63
 5 LNCIVAVSQMGIKNGKNDLPWPLNRPYRFRMTTSSVEGKQNLVINGKKTWFSIPEX 64
 64 NRPLKGRINLVLSRELKEPPQGAFTLSRLDALKLTERPELANKVDWVVGSSVYKE 123
 65 NRPLKGRINLVLSRELKEPPQGAFTLSRLDALKLTERPELANKVDWVVGSSVYKE 124
 124 AMNPHGLKLVTRINQDPESTFFPEIDLEKYLPLPYGVLSDVQEGKIKYKPEVYE 183
 125 AMNHLGHLKLVTRINQDPESTFFPEIDLEKYLPLPYGVLSDVQEGKIKYKPEVCE 184
 184 KND 186
 185 KOD 187

RESULT 12
 ADN99573
 ID ADN99573 standard; protein; 187 AA.

XX ADN99573;

XX 29-JUL-2004 (first entry)

XX Novel human protein sequence #389.

XX anti-inflammatory; dermatological; neuroprotective; immunomodulator;
 KM antibacterial; virucide; antipsoriatic; cytostatic; gene therapy;
 KM vaccine; inflammatory; CNS; immune disorder; cancer; psoriasis; diabetes;
 KM early aging; hormonal imbalance; ischemic heart disease;
 KM ulcerative colitis.

XX Homo sapiens.

XX WO2004038003-A2.

XX 06-MAY-2004.

XX 24-OCT-2003; 2003WO-US033947.

XX 25-OCT-2002; 2002US-0421061P.

XX 25-OCT-2002; 2002US-0421080P.

PR 25-OCT-2002; 2002US-0421552P.
 PR 25-OCT-2002; 2002US-0421614P.
 PR 30-OCT-2002; 2002US-0422177P.
 PR 30-OCT-2002; 2002US-0422178P.
 PR 15-NOV-2002; 2002US-042355P.
 PR 15-NOV-2002; 2002US-042584P.
 PR 15-NOV-2002; 2002US-0426394P.
 PR 15-NOV-2002; 2002US-0426430P.
 PR 15-NOV-2002; 2002US-0426916P.
 PR 27-NOV-2002; 2002US-0429224P.
 PR 27-NOV-2002; 2002US-0429275P.
 PR 27-NOV-2002; 2002US-0429302P.
 PR 27-NOV-2002; 2002US-0429328P.
 PR 27-NOV-2002; 2002US-0429651P.
 PR 04-DEC-2002; 2002US-0430645P.
 PR 04-DEC-2002; 2002US-0430651P.
 PR 04-DEC-2002; 2002US-0430657P.
 PR 04-DEC-2002; 2002US-0430663P.
 PR 04-DEC-2002; 2002US-0430668P.
 PR 04-DEC-2002; 2002US-0430684P.
 PR 05-DEC-2002; 2002US-0430937P.
 PR 05-DEC-2002; 2002US-0430965P.
 PR 05-DEC-2002; 2002US-0431458P.
 PR 12-DEC-2002; 2002US-0433251P.
 PR 12-DEC-2002; 2002US-0433500P.
 PR 13-DEC-2002; 2002US-0433316P.
 PR 13-DEC-2002; 2002US-0433318P.
 PR 23-DEC-2002; 2002US-0436236P.
 PR 03-JAN-2003; 2003US-0437514P.
 PR 17-JAN-2003; 2003US-0440820P.
 PR 18-JAN-2003; 2003US-0440821P.
 PR 18-APR-2003; 2003US-0463700P.
 PR 18-APR-2003; 2003US-0463708P.
 PR 18-APR-2003; 2003US-0463716P.
 PR 18-APR-2003; 2003US-0463732P.
 PR 02-MAY-2003; 2003US-0467159P.
 PR 02-MAY-2003; 2003US-0467201P.
 PR 02-MAY-2003; 2003US-0467203P.
 PR 02-MAY-2003; 2003US-0467230P.
 PR 19-MAY-2003; 2003US-0471306P.
 PR 19-MAY-2003; 2003US-0471336P.
 PR 22-MAY-2003; 2003US-0472420P.
 PR 22-MAY-2003; 2003US-0472430P.
 PR 09-JUN-2003; 2003US-0476609P.
 PR 09-JUN-2003; 2003US-0476621P.
 PR 09-JUN-2003; 2003US-0476632P.
 PR 08-JUL-2003; 2003US-0476641P.
 PR 08-JUL-2003; 2003US-0485217P.
 PR 08-JUL-2003; 2003US-0485218P.
 PR 08-JUL-2003; 2003US-0485223P.
 PR 08-JUL-2003; 2003US-0485224P.
 PR 08-JUL-2003; 2003US-0485325P.
 PR 08-JUL-2003; 2003US-0485359P.
 PR 14-JUL-2003; 2003US-0486446P.
 PR 14-JUL-2003; 2003US-0486480P.
 PR 15-JUL-2003; 2003US-0486891P.
 PR 08-AUG-2003; 2003US-0486960P.
 PR 08-AUG-2003; 2003US-0493341P.
 PR 08-AUG-2003; 2003US-0493370P.
 PR 08-AUG-2003; 2003US-0493573P.
 PR 08-AUG-2003; 2003US-0493577P.

(FIVE-) FIVE PRIME THERAPEUTICS INC.

Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
 Halenbeck RF, Kothakota S, Lin H, Linnemann T, Pierce K, Wang Y;
 Wong JGP, Wu G, Zhang H, Zeng C;

WPI: 2004-365511/34.

N-PSDB; ADN98789.

New nucleic acid molecules, useful in preparing a composition for
 treating or preventing e.g. inflammatory, CNS, bacterial or viral

PT disorders, cancer, psoriasis, diabetes, ischemic heart disease or
XX ulcerative colitis.

PS Claim 14; SEQ ID NO 1173; 532pp; English.

XX The invention relates to a nucleic acid molecule comprising a
CC polynucleotide sequence or its complement that encodes a polypeptide. The
CC nucleic acid is useful in preparing a composition for treating or
CC preventing inflammatory, CNS, immune, bacterial or viral disorder,
CC cancer, psoriasis, diabetes, early aging, hormonal imbalance, ischemic
CC heart disease or ulcerative colitis. This sequence corresponds to a
XX protein of the invention.

SQ Sequence 187 AA;

Query Match 89.5%; Score 875; DB 8; Length 187;
Best Local Similarity 92.9%; Pred. No. 1.8e-87;
Matches 170; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 LNCIVAVSQNMIGKNGDLPWPFRLNRFYFQRMFTTSSVEGKQNLVIMGKKTWFSIPEK 63
DB 5 LNCIVAVSQNMIGKNGDLPWPFRLNRFYFQRMFTTSSVEGKQNLVIMGKKTWFSIPEK 64
QY 64 NRPLKGRINLVLSRELKEPPQGAHFLSRLDDALKLTEPELANKVDMVIVGSSVYKE 123
DB 65 NRPLKGRINLVLSRELKEPPQGAHFLSRLDDALKLTEPELANKVDMVIVGSSVYKE 124
QY 124 ANNHGHLKLVTRIMQDFSDTFFPEIDLEKYKLLPEYGVLSVQVEEKGIYKFEVYE 183
DB 125 ANNHGHLKLVTRIMQDFSDTFFPEIDLEKYKLLPEYGVLSVQVEEKGIYKFEVCE 184
QY 184 KND 186
DB 185 KDD 187

RESULT 13

AAP40064
ID AAP40064 standard; protein; 186 AA.

XX AAP40064;

XX 09-JAN-1992 (first entry)

XX Sequence of dihydrofolate reductase (DHFR 3T6-R400), a DHFR enzyme
XX produced by a mutant line of mouse fibroblast cells.

XX Genetic marker; drug resistance; decreased methotrexate affinity.

XX Mus musculus.

XX Key Location/Qualifiers

FT Misc-difference 22 /note= "Leu in wt. DHFR"

XX EP117060-A.

XX 29-AUG-1984.

XX 18-JAN-1984; 84EP-00300300.

XX 19-JAN-1983; 83US-00459151.

XX (GETH) GENENTECH INC.

XX Levinson AD, Simonsen CC, Yelverton EM;

XX WPI; 1984-214789/35.

XX N-PSDB; AAN40061.

XX Plasmid with DNA coding for dihydro-folate reductase protein - opt. with
XX sequence encoding heterologous protein operatively linked.

PS Disclosure; Fig 1b; 52pp; English.

XX DHFR 3T6-R400 has a low binding affinity for methotrexate (MTX) a known
CC inhibitor of DHFR. The present invention thus enables growth of wild type
CC cells transformed with sequences coding for the modified DHFR at MTX
CC concentrations which would ordinarily be lethal. It permits detection of
CC cells that have been transformed with a vector, also including the coding
CC sequence for a desired heterologous protein

XX Sequence 186 AA;

Query Match 89.4%; Score 874; DB 1; Length 186;
Best Local Similarity 88.7%; Pred. No. 2.3e-87;
Matches 165; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 VSLNCIVAVSQNMIGKNGDLPWPFRLNRFYFQRMFTTSSVEGKQNLVIMGKKTWFSI 60
DB 1 VRPLNCIVAVSQNMIGKNGDLPWPFRLNRFYFQRMFTTSSVEGKQNLVIMGKKTWFSI 60
QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRLDDALKLTEPELANKVDMVIVGSSV 120
DB 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRLDDALKLTEPELANKVDMVIVGSSV 120
QY 121 YKEAMNHGHLKLVTRIMQDFSDTFFPEIDLEKYKLLPEYGVLSVQVEEKGIYKFE 180
DB 121 YQEAMNQGHLLRFLVTRIMQDFSDTFFPEIDLEKYKLLPEYGVLSVQVEEKGIYKFE 180
QY 181 VYKND 186
DB 181 VYKXD 186

RESULT 14

AAM41688
ID AAM41688 standard; protein; 198 AA.

XX AAM41688;

XX 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 6619.

XX Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-004711275.

XX 21-JAN-2000; 2000US-00498725.

XX 25-APR-2000; 2000US-0052317.

XX 20-JUN-2000; 2000US-00598042.

XX 19-JUL-2000; 2000US-00820312.

XX 03-AUG-2000; 2000US-00853450.

XX 14-SEP-2000; 2000US-00662191.

XX 19-OCT-2000; 2000US-00693036.

XX 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

XX Wang J, Wang Z, Wehrman T, Xu C, Xue AU, Yang Y, Zhang J, Zhao QA;

XX Zhou P, Goodrich R, Drmanac RT;

DR WPI; 2001-442253/47.
 DR N-PSDB; AAI60844.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.
 XX
 PS Example 2; SEQ ID NO 6619; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
 CC encoded polypeptides (AAM38642-AAAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilization of the activities such as: Immune system suppression,
 CC Acetylcholinesterase activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification
 XX
 SQ Sequence 198 AA;
 Query Match 89.4%; Score 874; DB 4; Length 198;
 Best Local Similarity 92.3%; Pred. No. 2.6e-87;
 Matches 169; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 QY 4 LNCIVAVSQNMIGKNGDLPWPFLENEFRYQRMVTTSSVEGKQNLVIMGKKTWFSIPEK 63
 DB 16 LNCIVAVSQNMIGKNGDLPWPFLENEFRYQRMVTTSSVEGKQNLVIMGKKTWFSIPEK 75
 QY 64 NRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDMMWIVGSSVYKE 123
 DB 76 NRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDMMWIVGSSVYKE 135
 QY 124 AMNHGHLKLVFTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSDVQEEKIKYKFEVE 183
 DB 136 AMNHGHLKLVFTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSDVQEEKIKYKFEVE 195
 QY 184 KND 186
 DB 196 KDD 198
 RESULT 15
 AAR07470
 TO AAR07470 standard; protein; 204 AA.
 AC AAR07470;
 XX
 DT 25-MAR-2003 (revised)
 DT 29-JAN-1991 (first entry)
 XX
 DE Transcript of plasmid pDS781/RBSII, 6xHis under the control of RBSII.
 XX
 KW IFN-gamma receptor; autoimmune disease; multiple sclerosis;
 KW hypersensitivity.
 XX
 OS Homo sapiens.
 XX
 PN EP393502-A.
 XX
 PD 24-OCT-1990.
 XX
 PF 11-APR-1990; 90EP-00106992.
 XX
 DR 19-APR-1989; 89EP-00810295.
 XX
 PA (HOFF) HOFFMANN-LA ROCHE AG.
 XX

PI Fountoulak M, Garotta G, Stuber D;
 XX WPI; 1990-322042/43.
 DR N-PSDB; AAO06305.
 XX
 PT Soluble interferon-gamma receptors - for treating auto-immune diseases,
 PT chronic inflammations, etc.
 XX
 PS Disclosure; Fig 12; 174pp; English.
 XX
 CC IFN-gamma is a therapeutically active agent in the treatment of
 CC autoimmune disease, allograft transplant rejections, multiple sclerosis,
 CC chronic inflammations and delayed hypersensitivity. It is also useful in
 CC identifying IFN-gamma agonists and antagonists. See also AAO06301.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 204 AA;
 Query Match 89.4%; Score 874; DB 2; Length 204;
 Best Local Similarity 89.7%; Pred. No. 2.7e-87;
 Matches 165; Conservative 12; Mismatches 7; Indels 0; Gaps 0;
 QY 1 VGSNCIVAVSQNMIGKNGDLPWPFLENEFRYQRMVTTSSVEGKQNLVIMGKKTWFSI 60
 DB 16 VRELNCIVAVSQNMIGKNGDLPWPFLENEFRYQRMVTTSSVEGKQNLVIMGKKTWFSI 75
 QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDMMWIVGSSV 120
 DB 76 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDMMWIVGSSV 135
 QY 121 YEAMNHGHLKLVFTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSDVQEEKIKYKFE 180
 DB 136 YQEAAMNHGHLKLVFTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSDVQEEKIKYKFE 195
 QY 181 VYEK 184
 DB 196 VYEK 199
 Search completed: November 19, 2004, 13:52:23
 Job time : 160 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 13:48:23 ; Search time 39 Seconds
(without alignments)
316.286 Million cell updates/sec

Title: US-10-650-417-7

Perfect score: 978

Sequence: 1 VGLNCIVAVSQNMIGKNG.....SDVQEKGIKYKFEVYEKND 186

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata1/1/aa/5A_COMB.pep:*
2: /cgn2_6/prodata1/1/aa/5B_COMB.pep:*
3: /cgn2_6/prodata1/1/aa/6A_COMB.pep:*
4: /cgn2_6/prodata1/1/aa/6B_COMB.pep:*
5: /cgn2_6/prodata1/1/aa/6C_COMB.pep:*
6: /cgn2_6/prodata1/1/aa/6D_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	978	100.0	186	4	US-09-142-530C-7
2	956	97.8	186	3	US-09-230-637-36
3	892	91.2	187	3	US-09-347-878-28
4	880	90.0	187	1	US-08-644-6648-19
5	880	90.0	187	2	US-08-761-277A-19
6	880	90.0	187	5	PCI-US94-00658-3
7	874	89.4	471	1	US-08-257-341-9
8	874	89.4	524	3	US-08-557-210A-3
9	874	89.4	539	3	US-08-557-210A-4
10	874	89.4	539	3	US-08-557-210A-5
11	864	88.3	193	1	US-08-192-479-2
12	864	88.3	193	1	US-08-637-508-2
13	864	88.3	193	1	US-08-417-791-2
14	864	88.3	193	5	PCI-US96-04546-2
15	864	88.3	297	4	US-10-030-031A-2
16	864	88.3	368	3	US-09-433-428D-58
17	864	88.3	439	3	US-09-433-428D-57
18	862	88.1	186	3	US-09-230-637-37
19	807	82.5	187	3	US-09-230-637-35
20	544.5	55.7	115	6	5164490-6
21	472.5	48.3	210	2	US-08-770-379-1
22	472.5	48.3	210	3	US-09-230-637-23
23	398	40.7	182	3	US-09-230-637-38
24	293.5	30.0	206	6	5164490-1
25	284	29.0	612	4	US-09-203-895-3
26	249	25.5	194	4	US-09-248-796A-20937
27	239	24.4	171	4	US-09-252-991A-27929

28	224	22.9	227	3	US-08-213-419B-13	Sequence 13, Appl
29	223.5	22.9	168	3	US-08-990-791-9	Sequence 9, Appli
30	223.5	22.9	168	4	US-09-372-591-9	Sequence 9, Appli
31	210.5	21.5	197	4	US-09-107-532A-4134	Sequence 4134, Ap
32	201.5	20.6	165	4	US-09-107-532A-7262	Sequence 7262, Ap
33	201.5	20.6	165	4	US-09-134-000C-5700	Sequence 5700, Ap
34	193	19.7	160	3	US-08-990-791-8	Sequence 8, Appli
35	193	19.7	160	4	US-09-372-591-8	Sequence 8, Appli
36	186.5	19.1	180	4	US-09-328-352-8063	Sequence 8063, Ap
37	182.5	18.7	176	4	US-09-540-236-2589	Sequence 2589, Ap
38	179	18.3	181	3	US-08-990-791-2	Sequence 2, Appli
39	179	18.3	181	3	US-08-990-791-12	Sequence 12, Appli
40	179	18.3	181	4	US-09-372-591-2	Sequence 12, Appli
41	179	18.3	181	4	US-09-372-591-12	Sequence 12, Appli
42	172	17.6	159	4	US-09-489-039A-12328	Sequence 12328, A
43	169	17.3	160	3	US-08-809-326A-14	Sequence 14, Appl
44	169	17.3	160	4	US-09-689-914A-14	Sequence 14, Appl
45	169	17.3	160	4	US-09-689-913A-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-09-142-530C-7

; Sequence 7, Application US/09142530C

; Patent No. 6642043

; GENERAL INFORMATION:

; APPLICANT: Bertino, Joseph R

; APPLICANT: Erican-Abali, Emine

; APPLICANT: Banerjee, Debabrata

; APPLICANT: Mineishi, Shin

; APPLICANT: Sadelain, Michel

; TITLE OF INVENTION: Double Mutants of Dihydrofolate Reductase and Methods of Using

; TITLE OF INVENTION: Same

; FILE REFERENCE: MSK.P-007

; CURRENT APPLICATION NUMBER: US/09/142.530C

; PRIOR FILING DATE: 1999-01-20

; PRIOR APPLICATION NUMBER: PCT/US97/03873

; PRIOR FILING DATE: 1997-03-12

; PRIOR APPLICATION NUMBER: US 60/013,270

; PRIOR FILING DATE: 1996-03-12

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 7

; LENGTH: 186

; TYPE: PRT

; ORGANISM: human

US-09-142-530C-7

Query Match 100.0%; Score 978; DB 4; Length 186;

Best Local Similarity 100.0%; Pred. No. 2.2e-103;

Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	VGLNCIVAVSQNMIGKNGDLPWFLRNEFRYQRTTSSVEGKQNLVIMGKKTWFSI	60
Db	1	VGLNCIVAVSQNMIGKNGDLPWFLRNEFRYQRTTSSVEGKQNLVIMGKKTWFSI	60
Qy	61	PEKNRPLKGRINLVLSRELKEPPQCAHFLSLDDALKLTPQELANKVDWVIWGSSV	120
Db	61	PEKNRPLKGRINLVLSRELKEPPQCAHFLSLDDALKLTPQELANKVDWVIWGSSV	120
Qy	121	YKEAMNHPGHLKLFVTRIMQDPESDTFFPEIDLKYLPPYGVLSDVQEKGIKYKFE	180
Db	121	YKEAMNHPGHLKLFVTRIMQDPESDTFFPEIDLKYLPPYGVLSDVQEKGIKYKFE	180
Qy	181	VYEKND 186	
Db	181	VYEKND 186	

RESULT 2

US-09-230-637-36

Sequence 36, Application US/09230637

Patent No. 6264958

GENERAL INFORMATION:

APPLICANT: Hayward, Gary

APPLICANT: Nicholas, John

APPLICANT: Hardwick, J. Marie

APPLICANT: Reitz, Marvin

TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma

TITLE OF INVENTION: Associated Herpesvirus

FILE REFERENCE: 1107.78372

CURRENT APPLICATION NUMBER: US/09/230,637

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: 60/022,591

PRIOR FILING DATE: 1996-07-25

PRIOR APPLICATION NUMBER: PCT US 97/12931

PRIOR FILING DATE: 1997-07-24

NUMBER OF SEQ ID NOS: 62

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 36

LENGTH: 186

TYPE: PRT

ORGANISM: Homo sapiens

US-09-230-637-36

Query Match 97.8%; Score 956; DB 3; Length 186;

Best Local Similarity 98.4%; Pred. No. 7.1e-101;

Matches 183; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSONMGIGKNGDLPWPLRNEFRYFQEMTTSSVEGKQNLVINGKKTWFSI 60

DB 1 VGSNCIVAVSONMGIGKNGDLPWPLRNEFRYFQEMTTSSVEGKQNLVINGKKTWFSI 60

QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDVWVIVGSSV 120

DB 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDVWVIVGSSV 120

QY 121 YKEAMNHPGHLKLFVTRIMQDFESDTPPEIDLEKYKLLPEYPGVLSVQVEKGKIKYKPE 180

DB 121 YKEAMNHPGHLKLFVTRIMQDFESDTPPEIDLEKYKLLPEYPGVLSVQVEKGKIKYKPE 180

QY 181 VYEKND 186

DB 181 VYEKND 186

RESULT 3

US-09-347-878-28

Sequence 28, Application US/09347878C

Patent No. 6376210

GENERAL INFORMATION:

APPLICANT: Yuan, Chong

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES

FILE REFERENCE: 25885-1451

CURRENT APPLICATION NUMBER: US/09/347,878C

PRIOR FILING DATE: 1999-07-06

NUMBER OF SEQ ID NOS: 75

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 28

LENGTH: 187

TYPE: PRT

ORGANISM: Cricetus sp.

US-09-347-878-28

Query Match

Best Local Similarity 91.3%; Score 892; DB 3; Length 187;

Matches 166; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSONMGIGKNGDLPWPLRNEFRYFQEMTTSSVEGKQNLVINGKKTWFSI 60

DB 2 VRLNCIVAVSONMGIGKNGDLPWPLRNEFRYFQEMTTSSVEGKQNLVINGKKTWFSI 61

QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDVWVIVGSSV 120

Db 62 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDVWVIVGSSV 121

QY 121 YKEAMNHPGHLKLFVTRIMQDFESDTPPEIDLEKYKLLPEYPGVLSVQVEKGKIKYKPE 180

Db 122 YKEAMNHPGHLKLFVTRIMQDFESDTPPEIDLEKYKLLPEYPGVLSVQVEKGKIKYKPE 181

QY 181 VYEKND 186

Db 182 VYEKND 187

RESULT 4

US-08-644-664B-19

Sequence 19, Application US/08644664B

Patent No. 5776746

GENERAL INFORMATION:

APPLICANT: Denney Jr., Dan W.

TITLE OF INVENTION: Gene Amplification Methods

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States Of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/644,664B

FILING DATE: 01-MAY-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: GENITOPR-00912

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 187 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-644-664B-19

Query Match 90.0%; Score 880; DB 1; Length 187;

Best Local Similarity 89.2%; Pred. No. 3.3e-92;

Matches 166; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSONMGIGKNGDLPWPLRNEFRYFQEMTTSSVEGKQNLVINGKKTWFSI 60

DB 2 VRLNCIVAVSONMGIGKNGDLPWPLRNEFRYFQEMTTSSVEGKQNLVINGKKTWFSI 61

QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDVWVIVGSSV 120

DB 62 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDVWVIVGSSV 121

QY 121 YKEAMNHPGHLKLFVTRIMQDFESDTPPEIDLEKYKLLPEYPGVLSVQVEKGKIKYKPE 180

DB 122 YKEAMNHPGHLKLFVTRIMQDFESDTPPEIDLEKYKLLPEYPGVLSVQVEKGKIKYKPE 181

QY 181 VYEKND 186

DB 182 VYEKND 187

RESULT 5

US-08-761-277A-19

Sequence 19, Application US/08761277A
Patent No. 5972334
GENERAL INFORMATION:
APPLICANT: Denney Jr., Dan W.
TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And
TITLE OF INVENTION: Leukemia
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,277A
FILING DATE: 06-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/644,664
FILING DATE: 01-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: GENITOPE-02406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-00658-3

Query Match 90.0%; Score 880; DB 2; Length 187;
Best Local Similarity 89.2%; Pred. No. 3.3e-92;
Matches 166; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSQNGIGKNGDLPPFPLRNEPRYQRMFTTSSVEGKQNLVIMGKKTWFSI 60
DB 2 VRPLNCIVAVSQNGIGKNGDLPPFPLRNEPRYQRMFTTSSVEGKQNLVIMGKKTWFSI 61

QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRDLDAKLTEQPELANKVDWVWIVGGSSV 120
DB 62 PEKNRPLKDRINLVLSRELKEPPQGAHFLAKSLDLDALRLIEQPELANKVDWVWIVGGSSV 121

QY 121 YKEAMNHPGHLKLFVTRIMQDFESTFPPEIDLEKYKLLPEYPGVLSVQBEKGIKYKFE 180
DB 122 YQEANQPGLRLFVTRIMQDFESTFPPEIDLGKYKLLPEYPGVLSVQBEKGIKYKFE 181

QY 181 VYEKND 186
DB 182 VYEKND 187

RESULT 6
PCT-US94-00658-3
Sequence 3, Application PC/TUS9400658
GENERAL INFORMATION:
APPLICANT: Dörner, Andrew
APPLICANT: Fritsch, Edward
APPLICANT: Steininger, Robert
APPLICANT: Bush, Lawrence
TITLE OF INVENTION: MCSF-223 Amino Acid Process
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140-2387
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00658
FILING DATE: 12-JAN-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,141
FILING DATE: 13-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lazat, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI-5210
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-876-1170
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-00658-3

Query Match 90.0%; Score 880; DB 5; Length 187;
Best Local Similarity 89.2%; Pred. No. 3.3e-92;
Matches 166; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSQNGIGKNGDLPPFPLRNEPRYQRMFTTSSVEGKQNLVIMGKKTWFSI 60
DB 2 VRPLNCIVAVSQNGIGKNGDLPPFPLRNEPRYQRMFTTSSVEGKQNLVIMGKKTWFSI 61

QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRDLDAKLTEQPELANKVDWVWIVGGSSV 120
DB 62 PEKNRPLKDRINLVLSRELKEPPQGAHFLAKSLDLDALRLIEQPELANKVDWVWIVGGSSV 121

QY 121 YKEAMNHPGHLKLFVTRIMQDFESTFPPEIDLEKYKLLPEYPGVLSVQBEKGIKYKFE 180
DB 122 YQEANQPGLRLFVTRIMQDFESTFPPEIDLGKYKLLPEYPGVLSVQBEKGIKYKFE 181

QY 181 VYEKND 186
DB 182 VYEKND 187

RESULT 7
US-08-257-341-9
Sequence 9, Application US/08257341
Patent No. 5525491
GENERAL INFORMATION:
APPLICANT: HUSTON, JAMES S
APPLICANT: OPPERMANN, HERMANN
APPLICANT: TIMASHEFF, SERGE N
TITLE OF INVENTION: SERINE RICH PEPTIDE LINKER
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: CREATIVE BIOMOLECULES, INC./PATENT DEPT.
STREET: 35 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,341
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/842,149
FILING DATE:
APPLICATION NUMBER: US 07/662,226
FILING DATE: 27-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL ESQ, PAULA A
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: CRP-064CP
TELEPHONE: 617/248-7000 (ATTY)
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 471 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-257-341-9

Query Match 89.4%; Score 874; DB 1; Length 471;
Best Local Similarity 88.7%; Pred. No. 6.2e-91;
Matches 165; Conservative 12; Mismatches 9; Indels 0; Gaps 0;
QY 1 VGLNCIVAVSQNMIGKNGDLPWPFRLNEPRYFQRTTSSVEGKQNLVIMGKKTWFSI 60
DB 2 VRPLNCIVAVSQNMIGKNGDLPWPFRLNEPRYFQRTTSSVEGKQNLVIMGKKTWFSI 61
QY 61 PEKRNPLKGRINVLVLSRELKEPPGGAHFLSRSLDDALKLTEQPELANKVDMMWIVGSSV 120
DB 62 PEKRNPLKDRINIVLSRELKEPPGGAHFLAKSLDDALLRIEQPELASKVDMMWIVGSSV 121
QY 121 YKEAMNHPGHLKLFVTRIMQDFSDTFPEIDLEKYKLLPEYPGVLSDVQEEKGIKYKFE 180
DB 122 YQEAANNQGHRLFLVTRIMQDFSDTFPEIDLGKYLPEYPGVLSDVQEEKGIKYKFE 181
QY 181 VYEKND 186
DB 182 VYEKND 187

RESULT 8
US-08-557-210A-3
Sequence 3, Application US/08557210A
Patent No. 6114146
GENERAL INFORMATION:
APPLICANT: Herlitschka, Sabine
APPLICANT: Schlokot, Uwe
APPLICANT: Falkner, Falko Guenther
APPLICANT: Dörner, Friedrich
TITLE OF INVENTION: A fusion protein, a
TITLE OF INVENTION: transfected eukaryotic cell line, a method of producing foreign
TITLE OF INVENTION: proteins, a foreign protein preparation as well as a pharmaceu
TITLE OF INVENTION: composition
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,210A
FILING DATE: 14-NOV-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: A 2099/94
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, John P.
REGISTRATION NUMBER: 33,715
REFERENCE/DOCKET NUMBER: 040433/0142/SOPA
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 524 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-557-210A-3

Query Match 89.4%; Score 874; DB 3; Length 524;
Best Local Similarity 89.7%; Pred. No. 7.2e-91;
Matches 165; Conservative 12; Mismatches 7; Indels 0; Gaps 0;
QY 1 VGLNCIVAVSQNMIGKNGDLPWPFRLNEPRYFQRTTSSVEGKQNLVIMGKKTWFSI 60
DB 2 VRPLNCIVAVSQNMIGKNGDLPWPFRLNEPRYFQRTTSSVEGKQNLVIMGKKTWFSI 61
QY 61 PEKRNPLKGRINVLVLSRELKEPPGGAHFLSRSLDDALKLTEQPELANKVDMMWIVGSSV 120
DB 62 PEKRNPLKDRINIVLSRELKEPPGGAHFLAKSLDDALLRIEQPELASKVDMMWIVGSSV 121
QY 121 YKEAMNHPGHLKLFVTRIMQDFSDTFPEIDLEKYKLLPEYPGVLSDVQEEKGIKYKFE 180
DB 122 YQEAANNQGHRLFLVTRIMQDFSDTFPEIDLGKYLPEYPGVLSDVQEEKGIKYKFE 181
QY 181 VYEKND 184
DB 182 VYEKND 185

RESULT 9
US-08-557-210A-4
Sequence 4, Application US/08557210A
Patent No. 6114146
GENERAL INFORMATION:
APPLICANT: Herlitschka, Sabine
APPLICANT: Schlokot, Uwe
APPLICANT: Falkner, Falko Guenther
APPLICANT: Dörner, Friedrich
TITLE OF INVENTION: An expression plasmid, a fusion protein, a
TITLE OF INVENTION: transfected eukaryotic cell line, a method of producing foreign
TITLE OF INVENTION: proteins, a foreign protein preparation as well as a pharmaceu
TITLE OF INVENTION: composition
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,210A


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/
/ FILING DATE: 14-NOV-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION NUMBER: A 2099/94
/ APPLICATION DATA:
/ FILING DATE: 14-NOV-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: ISACSON, John P.
/ REGISTRATION NUMBER: 33,715
/ REFERENCE/DOCKET NUMBER: 040433/0142/SOPA
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 539 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: Peptide
/ LOCATION: 192..196
/ OTHER INFORMATION: /note= "Glycin Spacer"
/
US-08-557-210A-4

Query Match 89.4%; Score 874; DB 3; Length 539;
Best Local Similarity 89.7%; Pred. No. 7.5e-91;
Matches 165; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 1 VGLNCIVAVSONMGIGKNGDLPWPFRLNRPYFORMTTSSVEGKQNLVIMGKKTWFSI 60
Db 2 VRPLNCIVAVSONMGIGKNGDLPWPFRLNRPYFORMTTSSVEGKQNLVIMGKKTWFSI 61
QY 61 PEKRPPLKGRINLVLSRELKEPPQGAHFLSLDDALKLTQPELANKYDVMWIVGSSV 120
Db 62 PEKRPPLKGRINLVLSRELKEPPQGAHFLSLDDALKLTQPELANKYDVMWIVGSSV 121
QY 121 YKEAMNHPGHLKLVTRIMQFESDTFFPEIDLEKYKLLPYPGVLSDVQBEKGIKYKFE 180
Db 122 YQEMANQPGHLRLFVTRIMQFESDTFFPEIDLGKYLLEPYPGVLSDVQBEKGIKYKFE 181
QY 181 VYEK 184
Db 182 VYEK 185

RESULT 10
US-08-557-210A-5
/ Sequence 5, Application US/08557210A
/ Patent No. 6114146
/ GENERAL INFORMATION:
/ APPLICANT: Herlitschka, Sabine
/ APPLICANT: Schlokot, Uwe
/ APPLICANT: Falkner, Falko Guenther
/ APPLICANT: Dornier, Friedrich
/ TITLE OF INVENTION: An expression plasmid, a fusion protein, a
/ TITLE OF INVENTION: transfected eukaryotic cell line, a method of producing foreign
/ TITLE OF INVENTION: proteins, a foreign protein preparation as well as a pharmaceu
/ TITLE OF INVENTION: composition
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner
/ STREET: 3000 K Street, N.W., Suite 500
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20007-5109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30

/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/557,210A
/ FILING DATE: 14-NOV-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: A 2099/94
/ FILING DATE: 14-NOV-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: ISACSON, John P.
/ REGISTRATION NUMBER: 33,715
/ REFERENCE/DOCKET NUMBER: 040433/0142/SOPA
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 539 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: Peptide
/ LOCATION: 190..194
/ OTHER INFORMATION: /note= "Prolin Spacer"
/
US-08-557-210A-5

Query Match 89.4%; Score 874; DB 3; Length 539;
Best Local Similarity 89.7%; Pred. No. 7.5e-91;
Matches 165; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 1 VGLNCIVAVSONMGIGKNGDLPWPFRLNRPYFORMTTSSVEGKQNLVIMGKKTWFSI 60
Db 2 VRPLNCIVAVSONMGIGKNGDLPWPFRLNRPYFORMTTSSVEGKQNLVIMGKKTWFSI 61
QY 61 PEKRPPLKGRINLVLSRELKEPPQGAHFLSLDDALKLTQPELANKYDVMWIVGSSV 120
Db 62 PEKRPPLKGRINLVLSRELKEPPQGAHFLSLDDALKLTQPELANKYDVMWIVGSSV 121
QY 121 YKEAMNHPGHLKLVTRIMQFESDTFFPEIDLEKYKLLPYPGVLSDVQBEKGIKYKFE 180
Db 122 YQEMANQPGHLRLFVTRIMQFESDTFFPEIDLGKYLLEPYPGVLSDVQBEKGIKYKFE 181
QY 181 VYEK 184
Db 182 VYEK 185

RESULT 11
US-08-192-479-2
/ Sequence 2, Application US/08192479
/ Patent No. 5538862
/ GENERAL INFORMATION:
/ APPLICANT: Wu, Peipei
/ APPLICANT: Dohmen, Jurgen
/ APPLICANT: Johnston, Jennifer
/ APPLICANT: Varshevsky, Alexander
/ TITLE OF INVENTION: HEAT-INDUCIBLE N-DEGRON
/ NUMBER OF SEQUENCES: 2
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Kevin M. Farrell
/ STREET: P.O. Box 999
/ CITY: York Harbor
/ STATE: Maine
/ COUNTRY: USA
/ ZIP: 03911
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/192,479

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Farrell, Kevin M.

REGISTRATION NUMBER: 35,505

REFERENCE/DOCKET NUMBER: CIT9301

TELECOMMUNICATION INFORMATION:

TELEPHONE: (207) 363-0558

TELEFAX: (207) 363-0528

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 193 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-192-479-2

Query Match 88.3%; Score 864; DB 1; Length 193;

Best Local Similarity 88.2%; Pred. No. 2.3e-90;

Matches 164; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 VGLNCIVAVSONMGIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVIMGKKTWFSI 60

DB 8 VRPLNCIVAVSONMGIGKNGDLPWPLRNEFKYFORMTTSSVEGKQNLVIMGKKTWFSI 67

QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDALKLTPQELANKVDVWVIYGGSSV 120

DB 68 PEKNRLLKDRINLVLSRELKEPPRGAHFLAKSLDALKLIEQPELASKVDVWVIYGGSSV 127

QY 121 YXEAMNHPGHLKLFVTRINMQPFESDTFFPEIDLEKYKLLPEYPGVLSVQVEKGIKYKFE 180

DB 128 YQEMNQGHLLKLFVTRINMQPFESDTFFPEIDLGKYLPEYPGVLSVQVEKGIKYKFE 187

QY 181 VYEKND 186

DB 188 VYEKND 193

QY 181 VYEKND 186

DB 188 VYEKND 193

QY 181 VYEKND 186

DB 188 VYEKND 193

RESULT 12

US-08-637-508-2

Sequence 2, Application US/08637508

Patent No. 5705387

GENERAL INFORMATION:

APPLICANT: Wu, Peipei

APPLICANT: Dohmen, Jurgen

APPLICANT: Varshavsky, Alexander

TITLE OF INVENTION: HEAT-INDUCIBLE N-DEGRON

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kevin M. Farrell

STREET: P.O. Box 999

CITY: York Harbor

STATE: Maine

COUNTRY: USA

ZIP: 03911

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/637,508

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/192,479

FILING DATE: 04-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: Farrell, Kevin M.

REGISTRATION NUMBER: 35,505

REFERENCE/DOCKET NUMBER: CIT9301D

TELECOMMUNICATION INFORMATION:

TELEPHONE: (207) 363-0558

TELEFAX: (207) 363-0528

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 193 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-637-508-2

Query Match 88.3%; Score 864; DB 1; Length 193;

Best Local Similarity 88.2%; Pred. No. 2.3e-90;

Matches 164; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 VGLNCIVAVSONMGIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVIMGKKTWFSI 60

DB 8 VRPLNCIVAVSONMGIGKNGDLPWPLRNEFKYFORMTTSSVEGKQNLVIMGKKTWFSI 67

QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDALKLTPQELANKVDVWVIYGGSSV 120

DB 68 PEKNRLLKDRINLVLSRELKEPPRGAHFLAKSLDALKLIEQPELASKVDVWVIYGGSSV 127

QY 121 YXEAMNHPGHLKLFVTRINMQPFESDTFFPEIDLEKYKLLPEYPGVLSVQVEKGIKYKFE 180

DB 128 YQEMNQGHLLKLFVTRINMQPFESDTFFPEIDLGKYLPEYPGVLSVQVEKGIKYKFE 187

QY 181 VYEKND 186

DB 188 VYEKND 193

QY 181 VYEKND 186

DB 188 VYEKND 193

QY 181 VYEKND 186

DB 188 VYEKND 193

RESULT 13

US-08-417-791-2

Sequence 2, Application US/08417791

Patent No. 5763212

GENERAL INFORMATION:

APPLICANT: Johnston, Jennifer

APPLICANT: Varshavsky, Alexander

TITLE OF INVENTION: HEAT-INDUCIBLE N-DEGRON

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kevin M. Farrell

STREET: P.O. Box 999

CITY: York Harbor

STATE: Maine

COUNTRY: USA

ZIP: 03911

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/417,791

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/192,479

FILING DATE: 04-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: Farrell, Kevin M.

REGISTRATION NUMBER: 35,505

REFERENCE/DOCKET NUMBER: CIT9301

TELECOMMUNICATION INFORMATION:

TELEPHONE: (207) 363-0558

TELEFAX: (207) 363-0528

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 193 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-417-791-2

Query Match 88.3%; Score 864; DB 1; Length 193;
Best Local Similarity 88.2%; Pred. No. 2.3e-90;
Matches 164; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSQNMIGKNGDLPWPFLENEFRYQRMVTTSSVEGKQNLVINGKKTWFSI 60
DB 8 VRPLNCIVAVSQNMIGKNGDLPWPFLENEFRYQRMVTTSSVEGKQNLVINGKKTWFSI 67

QY 61 PEKNRPLKGRINILVLSRELKPPQGAHFLSRSLDDALKLTEQPELANKVDMVWIVGGSSV 120
DB 68 PEKNRLLKDRINILVLSRELKPPQGAHFLAKSLDDALRLIEQPELASKVDMVWIVGGSSV 127

QY 121 YKEAMNHPGHLKFVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSDVQBEKGKIKYKFE 180
DB 128 YQEAMNQPGHLRFLVTRIMQDFESDTFFPEIDLGKYLKLLPEYPGVLSDVQBEKGKIKYKFE 187

QY 181 VYEKND 186
DB 188 VYEKXD 193

RESULT 14

PCT-US96-04546-2

; Sequence 2, Application PC/TUS9604546
; GENERAL INFORMATION:
; APPLICANT: California Institute of Technology
; TITLE OF INVENTION: HEAT-INDUCIBLE N-DEGRON
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell
; STREET: P.O. Box 999
; City: York Harbor
; STATE: Maine
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/04546
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/417,791
; FILING DATE: 06-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: CIT9301A WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-04546-2

Query Match 88.3%; Score 864; DB 5; Length 193;
Best Local Similarity 88.2%; Pred. No. 2.3e-90;
Matches 164; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSQNMIGKNGDLPWPFLENEFRYQRMVTTSSVEGKQNLVINGKKTWFSI 60
DB 8 VRPLNCIVAVSQNMIGKNGDLPWPFLENEFRYQRMVTTSSVEGKQNLVINGKKTWFSI 67

QY 61 PEKNRPLKGRINILVLSRELKPPQGAHFLSRSLDDALKLTEQPELANKVDMVWIVGGSSV 120

DB 68 PEKNRLLKDRINILVLSRELKPPQGAHFLAKSLDDALRLIEQPELASKVDMVWIVGGSSV 127

QY 121 YKEAMNHPGHLKFVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSDVQBEKGKIKYKFE 180

DB 128 YQEAMNQPGHLRFLVTRIMQDFESDTFFPEIDLGKYLKLLPEYPGVLSDVQBEKGKIKYKFE 187

QY 181 VYEKND 186

DB 188 VYEKXD 193

RESULT 15

US-10-030-031A-2

; Sequence 2, Application US/100300031A
; Patent No. 6746847
; GENERAL INFORMATION:
; APPLICANT: Vermeer, Ceas
; TITLE OF INVENTION: Diagnostic Assay for Human Matrix
; FILE REFERENCE: 13176PCTUS
; CURRENT APPLICATION NUMBER: US/10/030,031A
; PRIOR FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/EP00/06173
; PRIOR FILING DATE: 2000-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protein encoded by Sequence 1 containing 6-His tag
; Patent No. 6746847
; OTHER INFORMATION: - DHFR - linker (=4 amino acids) - MGP
; US-10-030-031A-2

Query Match 88.3%; Score 864; DB 4; Length 297;
Best Local Similarity 89.1%; Pred. No. 4.3e-90;
Matches 164; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSQNMIGKNGDLPWPFLENEFRYQRMVTTSSVEGKQNLVINGKKTWFSI 60

DB 16 VRPLNSIVAVSQNMIGKNGDLPWPFLENEFRYQRMVTTSSVEGKQNLVINGKKTWFSI 75

QY 61 PEKNRPLKGRINILVLSRELKPPQGAHFLSRSLDDALKLTEQPELANKVDMVWIVGGSSV 120

DB 76 PEKNRLLKDRINILVLSRELKPPQGAHFLAKSLDDALRLIEQPELASKVDMVWIVGGSSV 135

QY 121 YKEAMNHPGHLKFVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSDVQBEKGKIKYKFE 180

DB 136 YQEAMNQPGHLRFLVTRIMQDFESDTFFPEIDLGKYLKLLPEYPGVLSDVQBEKGKIKYKFE 195

QY 181 VYEK 184

DB 196 VYEK 199

Search completed: November 19, 2004, 13:53:27
Job time : 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 13:52:32 ; Search time 144 Seconds
(without alignments)
457.415 Million cell updates/sec

Title: US-10-650-417-7
Perfect score: 978
Sequence: 1 VGSNCIVAVSQNMGIKNG.....SDVQEEKGIKYEVEYKND 186

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	968	99.0	187	17	US-10-733-878-503
3	880	90.0	187	9	US-09-925-664-19
4	880	90.0	187	11	US-09-925-192-19
5	878	89.8	187	15	US-10-421-285-3
6	867	88.7	187	15	US-10-381-898-8
7	864	88.3	297	17	US-10-932-734-2
8	862	88.1	187	15	US-10-421-285-4
9	587.5	60.1	188	15	US-10-421-285-2
10	313.5	32.7	189	14	US-10-369-493-5158
11	301	30.8	530	15	US-10-424-599-247813
12	300	30.7	579	15	US-10-425-114-49649
13	298	30.5	475	15	US-10-425-114-43022

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Sequence 247817, A	15	285	29.1	530	15	US-10-424-599-247817
Sequence 123579, A	16	284	29.0	584	16	US-10-437-963-129579
Sequence 3987, Ap	17	280	28.6	273	14	US-10-369-493-3987
Sequence 235501, A	18	273	27.9	523	17	US-10-425-115-295501
Sequence 14308, A	19	242.5	24.8	166	14	US-10-369-493-14308
Sequence 14586, A	20	242.5	24.8	166	14	US-10-369-493-14586
Sequence 14938, A	21	242.5	24.8	166	14	US-10-369-493-14938
Sequence 11559, A	22	242.5	24.8	167	14	US-10-369-493-11559
Sequence 13912, A	23	239	24.4	164	14	US-10-369-493-13912
Sequence 11779, A	24	239	24.4	168	9	US-09-815-242-11779
Sequence 66164, A	25	239	24.4	168	15	US-10-282-122A-66164
Sequence 17427, A	26	230.5	23.6	163	14	US-10-369-493-17427
Sequence 289105, A	27	228.5	23.4	167	17	US-10-425-115-289105
Sequence 2402, A	28	225	23.0	211	14	US-10-369-493-22402
Sequence 8688, Ap	29	220	22.5	158	14	US-10-369-493-8688
Sequence 70130, A	30	219	22.4	153	15	US-10-282-122A-70130
Sequence 19664, A	31	213.5	21.8	183	14	US-10-369-493-19664
Sequence 57433, A	32	212.5	21.7	175	15	US-10-282-122A-57433
Sequence 67697, A	33	206.5	21.1	154	15	US-10-282-122A-67697
Sequence 50482, A	34	206.5	21.1	167	15	US-10-282-122A-50482
Sequence 16949, A	35	205.5	21.0	171	14	US-10-369-493-16949
Sequence 37727, A	36	204.5	20.9	129	16	US-10-767-701-37727
Sequence 16480, A	37	203.5	20.8	160	14	US-10-369-493-16480
Sequence 65425, A	38	202.5	20.7	162	15	US-10-282-122A-65425
Sequence 49091, A	39	198	20.2	166	15	US-10-282-122A-49091
Sequence 4316, Ap	40	197	20.1	163	14	US-10-369-493-4316
Sequence 7072, Ap	41	197	20.1	163	14	US-10-369-493-7072
Sequence 19156, A	42	195	19.9	144	14	US-10-369-493-19156
Sequence 66094, A	43	194.5	19.9	162	15	US-10-282-122A-66094
Sequence 11147, A	44	192	19.6	160	9	US-09-815-242-11147
Sequence 58345, A	45	192	19.6	160	15	US-10-282-122A-58345

ALIGNMENTS

RESULT 1
US-10-421-285-5
; Sequence 5, Application US/10421285
; Publication No. US20040053836A1
; GENERAL INFORMATION:
; APPLICANT: MayerKucuk, Phillip
; APPLICANT: Banerjee, Debabrata
; APPLICANT: Bertino, Joseph R.
; TITLE OF INVENTION: Method for Modulating the Production of a Selected Protein In
; TITLE OF INVENTION: Vivo
; FILE REFERENCE: MSK P-053
; CURRENT APPLICATION NUMBER: US/10/421,285
; CURRENT FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: US 60/375,250
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 186
; TYPE: PRI
; ORGANISM: human
US-10-421-285-5

Query Match	100.0%	Score	978	DB	15	Length	186
Best Local Similarity	100.0%	Pred. No.	5.4e-93				
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Gaps	0						
Qy	1	VGSNCIVAVSQNMGIKNGDLPWPFRLNEFRYFQMTTSSVEGKQNLVIMGKKTWFSI	60				
Db	1	VGSNCIVAVSQNMGIKNGDLPWPFRLNEFRYFQMTTSSVEGKQNLVIMGKKTWFSI	60				
Qy	61	PEKNRLKGRINLVLSRELKEPQGAHFLUSRLDALKLTEPELANKVDMWIVGSSSV	120				
Db	61	PEKNRLKGRINLVLSRELKEPQGAHFLUSRLDALKLTEPELANKVDMWIVGSSSV	120				
Qy	121	YKEANNHPGHLKLVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSVQVEEKIKYKFE	180				

DB 121 YKEAMNHPGHLKLVTRIMQDFESDTFFPEIDLEKYKLLPYPGVLSDVQBEKGIKYKFE 180
QY 181 VYEKND 186
DB 181 VYEKND 186

RESULT 2

US-09-925-664-19
Sequence 503, Application US/10733878
Publication No. US20040224408A1
GENERAL INFORMATION:
APPLICANT: Jean-Philippe Girard
APPLICANT: Francois Amalric
APPLICANT: Myriam Rousigne
APPLICANT: Thomas Clouaire
TITLE OF INVENTION: THAP PROTEINS AS NUCLEAR RECEPTORS FOR
TITLE OF INVENTION: CHEMOKINES AND ROLES IN TRANSCRIPTIONAL REGULATION, CELL
TITLE OF INVENTION: PROMILFERATION AND CELL DIFFERENTIATION
FILE REFERENCE: BIOBANK 012A
CURRENT APPLICATION NUMBER: US/10/733,878
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 60/432699
PRIOR FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/485027
PRIOR FILING DATE: 2003-07-03
NUMBER OF SEQ ID NOS: 535
SOFTWARE: PaetSeq for Windows Version 4.0
SEQ ID NO 503
LENGTH: 187
TYPE: PRT
ORGANISM: Homo sapiens
US-10-733-878-503

Query Match 99.0%; Score 968; DB 17; Length 187;
Best Local Similarity 99.5%; Pred. No. 5.9e-92;
Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VGS LNCI VAVSQNMGI GKNGLPWPFLRNEFRYQRTMTTSSVVEGKQNLVIMGKKTWFSI 60
DB 2 VGS LNCI VAVSQNMGI GKNGLPWPFLRNEFRYQRTMTTSSVVEGKQNLVIMGKKTWFSI 61
QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLSDALKLTEQPELANKVDVWVIVGGSSV 120
DB 62 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLSDALKLTEQPELANKVDVWVIVGGSSV 121
QY 121 YKEAMNHPGHLKLVTRIMQDFESDTFFPEIDLEKYKLLPYPGVLSDVQBEKGIKYKFE 180
DB 122 YKEAMNHPGHLKLVTRIMQDFESDTFFPEIDLEKYKLLPYPGVLSDVQBEKGIKYKFE 181
QY 181 VYEKND 186
DB 182 VYEKND 187

RESULT 3

US-09-925-664-19
Sequence 19, Application US/09925664
Patent No. US20020160006A1
GENERAL INFORMATION:
APPLICANT: Denney, Jr., Dan W.
TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
CURRENT APPLICATION NUMBER: US/09/925,664
CURRENT FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/370,453
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: 08/644,664
PRIOR FILING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/761,277
PRIOR FILING DATE: 1996-12-06
NUMBER OF SEQ ID NOS: 80

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-925-664-19

Query Match 90.0%; Score 880; DB 9; Length 187;
Best Local Similarity 89.2%; Pred. No. 7.9e-83;
Matches 166; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
QY 1 VGS LNCI VAVSQNMGI GKNGLPWPFLRNEFRYQRTMTTSSVVEGKQNLVIMGKKTWFSI 60
DB 2 VRLNCI VAVSQNMGI GKNGLPWPFLRNEFRYQRTMTTSSVVEGKQNLVIMGKKTWFSI 61
QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLSDALKLTEQPELANKVDVWVIVGGSSV 120
DB 62 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLSDALKLTEQPELANKVDVWVIVGGSSV 121
QY 121 YKEAMNHPGHLKLVTRIMQDFESDTFFPEIDLEKYKLLPYPGVLSDVQBEKGIKYKFE 180
DB 122 YQEAAMNQGHLLFVTRIMQDFESDTFFPEIDLGKYLPEYPGVLSVQBEKGIKYKFE 181
QY 181 VYEKND 186
DB 182 VYEKND 187

RESULT 4

US-09-925-192-19
Sequence 19, Application US/09925192
Publication No. US20040096452A1
GENERAL INFORMATION:
APPLICANT: Denney, Jr., Dan W.
TITLE OF INVENTION: Vaccines for Treatment of Lymphoma and Leukemia
FILE REFERENCE: GENITOP-06493
CURRENT APPLICATION NUMBER: US/09/925,192
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19
LENGTH: 187
TYPE: PRT
ORGANISM: Mus musculus
US-09-925-192-19

Query Match 90.0%; Score 880; DB 11; Length 187;
Best Local Similarity 89.2%; Pred. No. 7.9e-83;
Matches 166; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
QY 1 VGS LNCI VAVSQNMGI GKNGLPWPFLRNEFRYQRTMTTSSVVEGKQNLVIMGKKTWFSI 60
DB 2 VRLNCI VAVSQNMGI GKNGLPWPFLRNEFRYQRTMTTSSVVEGKQNLVIMGKKTWFSI 61
QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLSDALKLTEQPELANKVDVWVIVGGSSV 120
DB 62 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLSDALKLTEQPELANKVDVWVIVGGSSV 121
QY 121 YKEAMNHPGHLKLVTRIMQDFESDTFFPEIDLEKYKLLPYPGVLSDVQBEKGIKYKFE 180
DB 122 YQEAAMNQGHLLFVTRIMQDFESDTFFPEIDLGKYLPEYPGVLSVQBEKGIKYKFE 181
QY 181 VYEKND 186
DB 182 VYEKND 187

RESULT 5

US-10-421-285-3
Sequence 3, Application US/10421285
Publication No. US20040053836A1
GENERAL INFORMATION:
APPLICANT: Mayerkuckuk, Phillip

APPLICANT: Banerjee, Debabrata
APPLICANT: Bertino, Joseph R.
TITLE OF INVENTION: Method for Modulating the Production of a Selected Protein In
TITLE OF INVENTION: Vivo
FILE REFERENCE: MSK-P-053
CURRENT APPLICATION NUMBER: US/10/421,285
CURRENT FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: US 60/375,250
PRIOR FILING DATE: 2002-04-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 187
TYPE: PRT
ORGANISM: rat
US-10-421-285-3

Query Match 89.8%; Score 878; DB 15; Length 187;
Best Local Similarity 88.7%; Pred. No. 1.3e-82;
Matches 165; Conservative 12; Mismatches 9; Indels 0; Gaps 0;
Qy 1 VGSNCIVAVSQNMIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVINGKKTWFSI 60
Db 2 VRPLNCIVAVSQNMIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVINGKKTWFSI 61
Qy 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTPQELANKVDMVWIVGSSV 120
Db 62 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTPQELANKVDMVWIVGSSV 121
Qy 121 YKEANHPGHLKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYGVLSVQEEKIKYKFE 180
Db 122 YQEANHPGHLKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYGVLSVQEEKIKYKFE 181
Qy 181 YVEKND 186
Db 182 VYEKND 187

RESULT 6

US-10-381-898-8
Sequence 8, Application US/10381898
Publication No. US2004008687A1
GENERAL INFORMATION:
APPLICANT: AZIMZAI, Yalda; BAUGHN, Mariah R.;
APPLICANT: BOROWSKY, Mark L.; DING, Li;
APPLICANT: DUGAN, Brendan; ELLIOTT, Vicki S.;
APPLICANT: GANDHI, Aneena R.; GRIFFIN, Jennifer A.;
APPLICANT: HAFALIA, April J.A.; ISON, Craig H.;
APPLICANT: KHAN, Farrah A.; LAL, Preeti G.;
APPLICANT: LEE, Ernestine A.; LU, Dying Aina M.;
APPLICANT: ARVIZU Chandra S.; POLICKY, Jennifer L.;
APPLICANT: RAMKUMAR, Jayalaxmi; RING, Huijun Z.;
APPLICANT: SANJANWALA, Madhusudan M.;
APPLICANT: TANG, Y. Tom; TRIBOLEY, Catherine M.;
APPLICANT: CHAWLA, Narinder K.; WALSH, Roderick T.;
APPLICANT: WARREN, Bridget; XU, Yuming;
APPLICANT: YANG, Junming; YAO, Monique; YUE, Henry
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
FILE REFERENCE: PI-0233 USN
CURRENT APPLICATION NUMBER: US/10/381,898
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: PCT/US01/30662
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: US 60/238,864
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/242,323
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/249,519
PRIOR FILING DATE: 2000-11-16

PRIOR APPLICATION NUMBER: US 60/252,834
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 60/250,567
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PERL Program
SEQ ID NO 8
LENGTH: 187
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 5521346CD1
US-10-381-898-8

Query Match 88.7%; Score 867; DB 15; Length 187;
Best Local Similarity 92.3%; Pred. No. 1.7e-81;
Matches 169; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
Qy 4 LNCIVAVSQNMIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVINGKKTWFSIPEK 63
Db 5 LNCIVAVSQNMIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVINGKKTWFSIPEK 64
Qy 64 NRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTPQELANKVDMVWIVGSSVYKE 123
Db 65 NRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTPQELANKVDMVWIVGSSVYKE 124
Qy 124 AMNHPGHLKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYGVLSVQEEKIKYKFEVYE 193
Db 125 AMNHPGHLKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYGVLSVQEEKIKYKFEVCE 184
Qy 184 KND 186
Db 185 KDD 187

RESULT 7

US-10-832-734-2
Sequence 2, Application US/10832734
Publication No. US20040197830A1
GENERAL INFORMATION:
APPLICANT: Vermeer, Cees
TITLE OF INVENTION: Diagnostic Assay for Human Matrix
FILE REFERENCE: 13176PCTUS
CURRENT APPLICATION NUMBER: US/10/832,734
CURRENT FILING DATE: 2004-04-26
PRIOR APPLICATION NUMBER: US/10/030,031A
PRIOR FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: PCT/EP00/06173
PRIOR FILING DATE: 2000-07-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 297
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Protein encoded by Sequence 1 containing 6-His tag
OTHER INFORMATION: - DHFR - linker (=4 amino acids) - MGF
US-10-832-734-2

Query Match 88.3%; Score 864; DB 17; Length 297;
Best Local Similarity 89.1%; Pred. No. 6.7e-81;
Matches 164; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
Qy 1 VGSNCIVAVSQNMIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVINGKKTWFSI 60
Db 16 VRPLNCIVAVSQNMIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVINGKKTWFSI 75
Qy 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTPQELANKVDMVWIVGSSV 120
Db 76 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTPQELANKVDMVWIVGSSV 135

121 YKEMNHGHLKLFVTRIMQDPESTFFPEIDLEKYKLLPEYGVLSVQVEKGKYYKE 180
 136 YCEAMNQCHLFLVTRIMQDPESTFFPEIDLGKYLPEYGVLSVQVEKGKYYKE 195

181 VYEKND 184
 196 VYEKND 199

RESULT 8

US-10-421-285-4
 Sequence 4, Application US/10421285
 Publication No. US20040053836A1
 GENERAL INFORMATION:
 APPLICANT: MayerKuckuk, Phillip
 APPLICANT: Banerjee, Debabrata
 APPLICANT: Bertino, Joseph R.
 TITLE OF INVENTION: Method for Modulating the Production of a Selected Protein In Vivo
 FILE REFERENCE: MSK.P-053
 CURRENT APPLICATION NUMBER: US/10/421,285
 PRIOR FILING DATE: 2003-04-22
 PRIOR APPLICATION NUMBER: US 60/375,250
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: Patent in version 3.2
 SEQ ID NO 4
 TYPE: PRT
 ORGANISM: mouse
 US-10-421-285-4

Query Match 88.1%; Score 862; DB 15; Length 187;
 Best Local Similarity 88.2%; Pred. No. 5.8e-81;
 Matches 164; Conservative 12; Mismatches 10; Indels 0; Gaps 0;
 1 VGLNCIVAVSQNMGIGKNGDLPWFLNRPYFORMTTSSVEGKQNLVIMGKKTWFSI 60
 2 VRLPLCIVAVSQNMGIGKNGDLPWFLNRPYFORMTTSSVEGKQNLVIMGKKTWFSI 61
 61 PEKNPLKGRINLVLSRELKEPPQGAHFLSLDLDALKTQPELANKVDVMVWIVGSSV 120
 62 PEKNPLKGRINLVLSRELKEPPQGAHFLSLDLDALKTQPELANKVDVMVWIVGSSV 121
 121 YKEMNHGHLKLFVTRIMQDPESTFFPEIDLEKYKLLPEYGVLSVQVEKGKYYKE 180
 122 YCEAMNQCHLFLVTRIMQDPESTFFPEIDLGKYLPEYGVLSVQVEKGKYYKE 181
 181 VYEKND 186
 182 VYEKND 187

RESULT 9

US-10-421-285-2
 Sequence 2, Application US/10421285
 Publication No. US20040053836A1
 GENERAL INFORMATION:
 APPLICANT: MayerKuckuk, Phillip
 APPLICANT: Banerjee, Debabrata
 APPLICANT: Bertino, Joseph R.
 TITLE OF INVENTION: Method for Modulating the Production of a Selected Protein In Vivo
 FILE REFERENCE: MSK.P-053
 CURRENT APPLICATION NUMBER: US/10/421,285
 PRIOR FILING DATE: 2003-04-22
 PRIOR APPLICATION NUMBER: US 60/375,250
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: Patent in version 3.2
 SEQ ID NO 2
 LENGTH: 188

TYPE: PRT
 ORGANISM: monkey
 US-10-421-285-2

Query Match 60.1%; Score 587.5; DB 15; Length 188;
 Best Local Similarity 58.2%; Pred. No. 1.7e-52;
 Matches 107; Conservative 34; Mismatches 40; Indels 3; Gaps 2;

3 SLNCIVAVSQNMGIGKNGDLPWFLNRPYFORMTTSSVEGKQNLVIMGKKTWFSI 62
 4 AVNCIVAVDEQIGIGKNGDLPWFLNRPYFORMTTSSVEGKQNLVIMGKKTWFSI 63
 63 KRPPLKGRINLVLSRELKEPPQGAHFLSLDLDALKTQPELANKVDVMVWIVGSSV 122
 64 KRPPLVNRINILVLSRELKEPPQGAHFLSLDLDALKTQPELANKVDVMVWIVGSSV 123
 123 EAMNHGHLKLFVTRIMQDPESTFFPEIDLEKYKLLPEYGVLSVQVEKGKYYKE 181
 124 SVLNYKCPKLYITRIMFSDCDVFFPSINFTEYLMSELPG--KDTNPEENGIKYKFOV 181
 182 YEKND 185
 182 YEKND 185

RESULT 10

US-10-369-493-5158
 Sequence 5158, Application US/10369493
 Publication No. US20030233675A1
 GENERAL INFORMATION:
 APPLICANT: Cao, Yongwei
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Goldman, Barry S.
 APPLICANT: Chen, Xianfeng
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO 5158
 LENGTH: 189
 TYPE: PRT
 ORGANISM: Caenorhabditis elegans
 US-10-369-493-5158

Query Match 32.7%; Score 319.5; DB 14; Length 189;
 Best Local Similarity 36.0%; Pred. No. 1e-24;
 Matches 64; Conservative 41; Mismatches 70; Indels 3; Gaps 2;

4 LNCIVAVSQNMGIGKNGDLPWFLNRPYFORMTTSSVEGKQNLVIMGKKTWFSI 63
 4 MNLIVAMDAGGIGKNGDLPWFLNRPYFORMTTSSVEGKQNLVIMGKKTWFSI 62
 64 NRPLKGRINLVLSRELKEPPQGAHFLSLDLDALKTQPELANKVDVMVWIVGSSV 123
 63 RRPLAGRLNVLNRQLPAKSDDDYIVANSLEAAMKLLSEPPFVDSIETWNIGGAIVDL 122
 124 AMNHGHLKLFVTRIMQDPESTFFPEIDLEKYKLL--PEYGVLSVQVEKGKYYKE 179
 123 ALRNLVDEIHTRIPKFNFEADVHLKSLDFSKVEKQVNAEVSSEISEFENGLAFEF 180

RESULT 11

US-10-424-599-247813
 Sequence 247813, Application US/10424599
 Publication No. US20040031072A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa Thomas J
 APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 247813
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_WRT3847_65805C.1.pep
US-10-424-599-247813

Query Match 30.8%; Score 301; DB 15; Length 530;
Best Local Similarity 33.2%; Pred. No. 3.3e-22;
Matches 66; Conservative 41; Mismatches 62; Indels 30; Gaps 5;

QY 2 GSLN-----CIVAVSQNMGIKNGDLPWPFLENERFYFORMTTTSSVEGKQNLVI 51
DB 15 GSVNPLNLTQYQVVAATQDWIGKDGKLPWR-LPTDLKFFKEITMKTSEFGKKAIV 73
QY 52 MGKKTWFSIPEKNRPLKGRINLVLSRELKEPPOGAHFLSR-----SLDDALKLTQEP 103
DB 74 MGRKTWESIPEYRPLSGRLNVLTR-----SGSFDIATAENNVICGSMSSALELLAAS 127
QY 104 ELANKVDVWIVGGSSVYKEAMNHPGHLKLFVTRIMQDFESDTPFPFIDLEKYKLLPEYP 163
DB 128 PYSLSIEKVFVIGGGQIFREALNVPGCCAIHLTEIQSSIECDTFMPPVDFTFIFR-----P 182
QY 164 GVLSDVOEEKIGIKYKFEVY 182
DB 183 WYSSFPKVENNIRYSFTTY 201

RESULT 12
US-10-425-114-49649
; Sequence 49649, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 49649
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3051-050-G2_FLI.pep
US-10-425-114-49649

Query Match 30.7%; Score 300; DB 15; Length 579;
Best Local Similarity 33.2%; Pred. No. 4.8e-22;
Matches 66; Conservative 41; Mismatches 62; Indels 30; Gaps 5;

QY 2 GSLN-----CIVAVSQNMGIKNGDLPWPFLENERFYFORMTTTSSVEGKQNLVI 51
DB 64 GSVNPLNLTQYQVVAATQDWIGKDGKLPWR-LPTDLKFFKEITMKTSEFGKKAIV 122
QY 52 MGKKTWFSIPEKNRPLKGRINLVLSRELKEPPOGAHFLSR-----SLDDALKLTQEP 103
DB 123 MGRKTWESIPEYRPLSGRLNVLTR-----SGSFDIATAENNVICGSMSSALELLAAS 176

QY 104 ELANKVDVWIVGGSSVYKEAMNHPGHLKLFVTRIMQDFESDTPFPFIDLEKYKLLPEYP 163
DB 177 PYSLSIEKVFVIGGGQIFREALNVPGCCAIHLTEIQSSIECDTFMPPVDFTFIFR-----P 231
QY 164 GVLSDVOEEKIGIKYKFEVY 182
DB 232 WYSSFPKVENNIRYSFTTY 250

RESULT 13

US-10-425-114-43022
; Sequence 43022, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 43022
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700746445_FLI.pep
US-10-425-114-43022

Query Match 30.5%; Score 298; DB 15; Length 475;

Best Local Similarity 33.2%; Pred. No. 5.9e-22;
Matches 66; Conservative 41; Mismatches 62; Indels 30; Gaps 5;

QY 2 GSLN-----CIVAVSQNMGIKNGDLPWPFLENERFYFORMTTTSSVEGKQNLVI 51
DB 85 GSVNPLNLTQYQVVAATQDWIGKDGKLPWR-LPTDLKFFKEITMKTSEFGKKAIV 143
QY 52 MGKKTWFSIPEKNRPLKGRINLVLSRELKEPPOGAHFLSR-----SLDDALKLTQEP 103
DB 144 MGRKTWESIPEYRPLSGRLNVLTR-----SGSFDIATAENNVICGSMSSALELLAAS 197
QY 104 ELANKVDVWIVGGSSVYKEAMNHPGHLKLFVTRIMQDFESDTPFPFIDLEKYKLLPEYP 163
DB 198 PYSLSIEKVFVIGGGQIFREALNVPGCCAIHLTEIQSSIECDTFMPPVDFTFIFR-----P 252
QY 164 GVLSDVOEEKIGIKYKFEVY 182
DB 253 WYSSFPKVENNIRYSFTTY 271

RESULT 14

US-10-437-963-197466
; Sequence 197466, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963

Search completed: November 19, 2004, 14:04:25
Job time : 145 secs

61 PEKNRPJUKDRINIVLSRELKEPQGAHFLAKSLDDALKLIEQFELADKVDWMIIVGSSV 120

121 YKEAMNHFGHKLFLVTRIMQDFSDTFFPEIDLEKYKLLPEYFGVLSDVQBEKGIKYKFE 180

121 YKEAMNQGHLRFLVTRIMQDFSDTFFPEIDLEKYKLLPEYFGVLSEVQBEKGIKYKFE 180

181 VYEK 184

181 VYEK 184

RESULT 3

S42445

EC 1.5.1.3 (cione A3-35) - Chinese hamster

Species: Cricetus griseus (Chinese hamster)

C7:Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 11-Jun-1999.

C:Accession: S42445

R:Meleard, P.W.; Davide, J.P.; Hession, C.A.; Scotto, K.W.

Mol. Cell. Biol. 4, 38-48, 1984

A:Title: Phenotypic expression in Escherichia coli and nucleotide sequence of two Chinese

A:Reference number: S42445; MUID:94141854; PMID:6366511

A:Accession: S42445

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-187 <MEL>

A:Cross-references: EMBL:K01164; NID:g191053; PIDN:AAA36974.1; PID:g304503

A>Note: the authors translated the codon AAC for residue 49 as ASP, CAG for residue 128

```

Query Match      89.6%; Score 876; DB 2; Length 187;
Best Local Similarity 89.7%; Pred. No. 1.2e-69;
Matches 165; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

1 VGSINCIIVASQNGIGKGGDLWPPELRNRPYRFRMTTSSVEGQKNLVINGKRTWFSI 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2 VRPLNCIVASQNGIGKGGDFPWPVLRNRPYRFRMTTSSVEGQKNLVINGKRTWFSI 61
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61 PEKNRPLKGRINLVLSREUKEPQGAHFLRSLSDDLALKLTQPELANKQDMVWIVGGSSV 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
62 PEKNRPLKGRINLVLSREUKEPQGAHFLRSLSDDLALKLTQPELANKQDMVWIVGGSSV 121
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
121 YKEANNPQGHILKLVTRINQDPESTDFPPEIDLEKYKLLPEYPGVLSVQBEKGIKYKFE 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
122 YKEANNPQGHILKLVTRINQDPESTDFPPEIDLEKYKLLPEYPRVLPEVQBEKGIKYKFE 181
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
181 VYEK 184
| | | |
182 VYEK 185
| | | |

RESULT 4
dihydrofolate reductase (EC 1.5.1.3), methotrexate-resistant - mouse

```

[illegible]

A;Residues: 1-13,'D','15-187 <S1M>
A;Cross-references: EMBL:X56066; NID:G50710; PIDN:CAA39544.1; PID:G50711
R;Crouse, G.F.; Simonsen, C.C.; McSwan, R.N.; Schimke, R.T.
J. Biol. Chem. 257, 7887-7897, 1982
A;Title: Structure of amplified normal and variant dihydrofolate reductase genes in mouse
A;Accession number: I48328; MUID:82213979; PMID:6282858
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-28 <RES>
A;Cross-references: EMBL:V00735; NID:G50701; PIDN:CAA24113.1; PID:G1619305
R;McGrogan, M.; Simonsen, C.C.; Smouse, D.T.; Farnham, P.J.; Schimke, R.T.
J. Biol. Chem. 260, 2307-2314, 1985
A;Title: Heterogeneity at the 5' termini of mouse dihydrofolate reductase mRNAs: Evidence
A;Reference number: I49672; MUID:85130969; PMID:2982814
A;Accession: I49672
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-3,'A','5-28 <R2>
A;Cross-references: GB:M10071; NID:G193331; PIDN:AAA37637.1; PID:G553915
R;Stone, D.; Paterson, S.J.; Raper, J.H.; Phillips, A.W.
J. Biol. Chem. 254, 480-488, 1979
A;Title: The amino acid sequence of dihydrofolate reductase from the mouse lymphoma L1210
A;Reference number: A92253; MUID:79109591; PMID:762074
A;Accession: A92253
A;Molecule type: protein
A;Residues: 2-31,'F','33-122,'EQ','125-127,'E','129-173,'D','175-187 <STO>
A;Experimental source: Lymphoma L1210 cells
R;Nunberg, J.H.; Kaufman, R.J.; Chang, A.C.Y.; Cohen, S.N.; Schimke, R.T.
Cell 19, 355-364, 1980
A;Title: Structure and genomic organization of the mouse dihydrofolate reductase gene.
A;Reference number: A90792; MUID:80132485; PMID:6244105
A;Accession: A90792
A;Molecule type: mRNA
A;Residues: 2-24;50-127;154-187 <NUN>
A;Note: the authors translated the codon GAG for residue 169 as Gly
R;Chang, A.C.Y.; Nunberg, J.; Kaufman, R.J.; Erlich, H.A.; Schimke, R.T.; Cohen, S.N.
Nature 275, 617-624, 1978
A;Title: Phenotypic expression in E.coli of a DNA sequence coding for mouse dihydrofolate
A;Reference number: I49632; MUID:79032141; PMID:360074
A;Accession: I49632
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-24 <RE3>
A;Cross-references: GB:M10722; NID:G192946; PIDN:AAA37524.1; PID:G192949
A;Accession: I49633
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 50-122,'E','124-127 <RE4>
A;Cross-references: GB:M10811; NID:G192947; PIDN:AAA37525.1; PID:G192950
R;Simonsen, C.C.; Levinson, A.D.
Proc. Natl. Acad. Sci. U.S.A. 80, 2495-2499, 1983
A;Title: Isolation and expression of an altered mouse dihydrofolate reductase cDNA.
A;Reference number: A21119; MUID:83195084; PMID:6573667
A;Accession: A21119
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 2-22,'F','24-31,'F','33-187 <S12>
A;Cross-references: GB:V00734; NID:G50699; PIDN:CAA24112.1; PID:G50700
C;Superfamily: Dihydrofolate reductase, type I dihydrofolate reductase homology
C;Keywords: methotrexate resistance; NADP; one-carbon metabolism; oxidoreductase
F;4-126/Domain: type I dihydrofolate reductase homology <DFR>
F;31,35,65,71/Binding site: substrate (Glu, Phe, Asn, Arg) #status predicted
Query Match 89.5%; Score 875; DB 1; Length 187;
Best Local Similarity 88.7%; Pred. No. 1,5e-69;
Matches 165; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
QY 1 VGSNCIVAVSQNMIGKNGDLFPWFLRNEFRYFORMTTSSVEGKQNLVINGKKTWFSI 60
DB 2 VRPLNCIVAVSQNMIGKNGDLFPWPLRNEFKYFORMTTSSVEGKQNLVINGRKTWFSI 61
QY 61 PEKNRPLKGRINLVLSRELKPPQGAHFLSRSLDDALKLTEQPELANKYVDWVWIVGGSSV 120

DB 62 PEKNRPLKGRINLVLSRELKPPQGAHFLAKSLDDALKLTEQPELASKVDMWVWIVGGSSV 121
QY 121 YKEAMNHPGHLKLFVTRIMQDPESDTFFPEIDLEKYKLLPEYPGVLSVDVQEEKGIKYKFE 180
DB 122 YQEAAMQPGHLKLFVTRIMQDPESDTFFPEIDLKYLKLLPEYPGVLSVDVQEEKGIKYKFE 181
QY 181 VYEKND 186
DB 182 VYEKND 187
RESULT 5
S42446
dihydrofolate reductase (EC 1.5.1.3) - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S42446; I48106
R;Weler, P.W.; Davids, J.P.; Hession, C.A.; Scotto, K.W.
Mol. Cell. Biol. 4, 38-48, 1984
A;Title: Phenotypic expression in Escherichia coli and nucleotide sequence of two Chinese
A;Reference number: S42445; MUID:84141864; PMID:6366511
A;Accession: S42446
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-187 <WEL>
A;Cross-references: UNIPROT:Q64742; EMBL:X01155; NID:G191058; PIDN:AAA36976.1; PID:G304
A;Note: the authors translated the codon AAC for residue 49 as Asp, CAG for residue 128
168 as Ser
R;Mitchell, P.J.; Carothers, A.M.; Han, J.H.; Harding, J.D.; Kas, E.; Venolia, L.; Chas
Mol. Cell. Biol. 6, 425-440, 1986
A;Title: Multiple transcription start sites, DNase I-hypersensitive sites, and an oppos
A;Reference number: I48106; MUID:87064325; PMID:3023846
A;Accession: I48106
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-45 <MIT>
A;Cross-references: GB:M13129; NID:G191060; PIDN:AAA51447.1; PID:G553839
C;Genetics:
A;Gene: DHFR
A;Introns: 29/2
C;Superfamily: type I dihydrofolate reductase; type I dihydrofolate reductase homology
C;Keywords: NADP; oxidoreductase
F;4-126/Domain: type I dihydrofolate reductase homology <DFR>
Query Match 89.5%; Score 875; DB 2; Length 187;
Best Local Similarity 89.7%; Pred. No. 1,5e-69;
Matches 165; Conservative 11; Mismatches 8; Indels 0; Gaps 0;
QY 1 VGSNCIVAVSQNMIGKNGDLFPWFLRNEFRYFORMTTSSVEGKQNLVINGKKTWFSI 60
DB 2 VRPLNCIVAVSQNMIGKNGDLFPWPLRNEFKYFORMTTSSVEGKQNLVINGRKTWFSI 61
QY 61 PEKNRPLKGRINLVLSRELKPPQGAHFLSRSLDDALKLTEQPELANKYVDWVWIVGGSSV 120
DB 62 PEKNRPLKGRINLVLSRELKPPQGAHFLAKSLDDALKLTEQPELADKYVDWVWIVGGSSV 121
QY 121 YKEAMNHPGHLKLFVTRIMQDPESDTFFPEIDLEKYKLLPEYPGVLSVDVQEEKGIKYKFE 180
DB 122 YQEAAMQPGHLKLFVTRIMQDPESDTFFPEIDLKYLKLLPEYPRVLPEVQEEKGIKYKFE 181
QY 181 VYEK 184
DB 182 VYEK 185
RESULT 6
RDPGD
dihydrofolate reductase (EC 1.5.1.3) - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 28-Feb-1980 #sequence_revision 28-Feb-1980 #text_change 16-Aug-2004
C;Accession: A00389
R;Smith, S.L.; Patrick, P.; Stone, D.; Phillips, A.W.; Burchall, J.J.

3. Biol. Chem. 254, 11475-11484, 1979
 A:Title: Porcine liver dihydrofolate reductase. Purification, properties, and amino acid
 A:Reference number: A00389; MUID:80049777; PMID:500653
 A:Accession: A00389

A:Molecule type: protein
 A:Residues: 1-186 <SMI>
 A:Cross-references: UNIPROT:P00377
 A:Experimental source: liver
 A:Note: Cys-162 may be modified in approximately 30% of the molecules
 C:Superfamily: Dihydrofolate reductase; type I dihydrofolate reductase homology
 C:Keywords: NADP; oxidoreductase
 F:3-125/Domain: type I dihydrofolate reductase homology <DPR>
 F:30,34,64,70/Binding site: substrate (Glu, Phe, Asn, Arg) #status predicted

Query Match 88.1%; Score 862; DB 1; Length 186;
 Best Local Similarity 88.2%; Pred. No. 2e-68;
 Matches 164; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSONMGIGKNGDLPWFLNRPYFQMTTSSVEGKQNLVIMGKKTWFSI 60
 PB 1 VRPLNCIVAVSONMGIGKNGDLPWFLNRPYFQMTTSSVEGKQNLVIMGKKTWFSI 60
 QY 61 PEKNRPLKGRINLVLSRELKPEPPQGAHFLSLDLDALXLTQPELANKVDMVMVIVGGSSV 120
 DB 61 PEKNRPLKGRINLVLSRELKPEPPQGAHFLSLDLDALXLTQPELANKVDMVMVIVGGSSV 120
 QY 121 YKEAMNHGHLKLFVTRINQDFESTFPPEIDLEKYLPLPYGVLSDVQBEKGIKYKFE 180
 DB 121 YKEAMNHGHLKLFVTRINQDFESTFPPEIDLEKYLPLPYGVLSDVQBEKGIKYKFE 180
 QY 181 VYEKND 186
 DB 181 VYEKND 186

RESULT 7
 ROBOD
 dihydrofolate reductase (EC 1.5.1.3) - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 15-Oct-1982 #sequence_revision 15-Oct-1982 #text_change 16-Aug-2004
 A:Accession: A00388
 A:Residues: 1-186 <LA1>
 A:Cross-references: UNIPROT:P00376
 A:Experimental source: liver
 A:Note: Cys-162 may be modified in approximately 30% of the molecules
 C:Superfamily: Dihydrofolate reductase; type I dihydrofolate reductase homology
 C:Keywords: NADP; oxidoreductase
 F:3-125/Domain: type I dihydrofolate reductase homology <DPR>
 F:30,34,64,70/Binding site: substrate (Glu, Phe, Asn, Arg) #status predicted

Query Match 87.1%; Score 852; DB 1; Length 186;
 Best Local Similarity 86.0%; Pred. No. 1.5e-67;
 Matches 160; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSONMGIGKNGDLPWFLNRPYFQMTTSSVEGKQNLVIMGKKTWFSI 60
 PB 1 VRPLNCIVAVSONMGIGKNGDLPWFLNRPYFQMTTSSVEGKQNLVIMGKKTWFSI 60
 QY 61 PEKNRPLKGRINLVLSRELKPEPPQGAHFLSLDLDALXLTQPELANKVDMVMVIVGGSSV 120
 DB 61 PEKNRPLKGRINLVLSRELKPEPPQGAHFLSLDLDALXLTQPELANKVDMVMVIVGGSSV 120
 QY 121 YKEAMNHGHLKLFVTRINQDFESTFPPEIDLEKYLPLPYGVLSDVQBEKGIKYKFE 180
 DB 121 YKEAMNHGHLKLFVTRINQDFESTFPPEIDLEKYLPLPYGVLSDVQBEKGIKYKFE 180
 QY 181 VYEKND 186
 DB 181 VYEKND 186

Db 181 VYEKND 186

RESULT 8

ROBOD
 dihydrofolate reductase (EC 1.5.1.3) - saimirine herpesvirus 1 (strain 11)
 C:Species: saimirine herpesvirus 1
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Aug-2004
 A:Accession: A29954; B36806
 A:Residues: 1-187 <TRI>
 A:Cross-references: UNIPROT:P00377
 A:Experimental source: liver
 A:Note: Cys-162 may be modified in approximately 30% of the molecules
 C:Superfamily: Dihydrofolate reductase; type I dihydrofolate reductase homology
 C:Keywords: NADP; oxidoreductase
 F:3-125/Domain: type I dihydrofolate reductase homology <DPR>
 F:30,34,64,70/Binding site: substrate (Glu, Phe, Asn, Arg) #status predicted

Query Match 88.1%; Score 862; DB 1; Length 186;
 Best Local Similarity 88.2%; Pred. No. 2e-68;
 Matches 164; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSONMGIGKNGDLPWFLNRPYFQMTTSSVEGKQNLVIMGKKTWFSI 60
 PB 1 VRPLNCIVAVSONMGIGKNGDLPWFLNRPYFQMTTSSVEGKQNLVIMGKKTWFSI 60
 QY 61 PEKNRPLKGRINLVLSRELKPEPPQGAHFLSLDLDALXLTQPELANKVDMVMVIVGGSSV 120
 DB 61 PEKNRPLKGRINLVLSRELKPEPPQGAHFLSLDLDALXLTQPELANKVDMVMVIVGGSSV 120
 QY 121 YKEAMNHGHLKLFVTRINQDFESTFPPEIDLEKYLPLPYGVLSDVQBEKGIKYKFE 180
 DB 121 YKEAMNHGHLKLFVTRINQDFESTFPPEIDLEKYLPLPYGVLSDVQBEKGIKYKFE 180
 QY 181 VYEKND 186
 DB 181 VYEKND 186

Query Match 82.5%; Score 807; DB 1; Length 187;
 Best Local Similarity 83.8%; Pred. No. 1.4e-63;
 Matches 155; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSONMGIGKNGDLPWFLNRPYFQMTTSSVEGKQNLVIMGKKTWFSI 60
 PB 1 VRPLNCIVAVSONMGIGKNGDLPWFLNRPYFQMTTSSVEGKQNLVIMGKKTWFSI 60
 QY 61 PEKNRPLKGRINLVLSRELKPEPPQGAHFLSLDLDALXLTQPELANKVDMVMVIVGGSSV 120
 DB 61 PEKNRPLKGRINLVLSRELKPEPPQGAHFLSLDLDALXLTQPELANKVDMVMVIVGGSSV 120
 QY 121 YKEAMNHGHLKLFVTRINQDFESTFPPEIDLEKYLPLPYGVLSDVQBEKGIKYKFE 180
 DB 121 YKEAMNHGHLKLFVTRINQDFESTFPPEIDLEKYLPLPYGVLSDVQBEKGIKYKFE 180
 QY 181 VYEKND 186
 DB 181 VYEKND 186

RESULT 9

ROBOD
 dihydrofolate reductase (EC 1.5.1.3) - saimirine herpesvirus 1 (strain 484-77)
 C:Species: saimirine herpesvirus 1
 C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 11-Jun-1999
 A:Accession: S14840
 A:Residues: 1-187 <TRI>
 A:Cross-references: UNIPROT:P00377
 A:Experimental source: liver
 A:Note: Cys-162 may be modified in approximately 30% of the molecules
 C:Superfamily: Dihydrofolate reductase; type I dihydrofolate reductase homology
 C:Keywords: NADP; oxidoreductase
 F:3-125/Domain: type I dihydrofolate reductase homology <DPR>
 F:30,34,64,70/Binding site: substrate (Glu, Phe, Asn, Arg) #status predicted

Query Match 87.1%; Score 852; DB 1; Length 186;
 Best Local Similarity 86.0%; Pred. No. 1.5e-67;
 Matches 160; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSONMGIGKNGDLPWFLNRPYFQMTTSSVEGKQNLVIMGKKTWFSI 60
 PB 1 VRPLNCIVAVSONMGIGKNGDLPWFLNRPYFQMTTSSVEGKQNLVIMGKKTWFSI 60
 QY 61 PEKNRPLKGRINLVLSRELKPEPPQGAHFLSLDLDALXLTQPELANKVDMVMVIVGGSSV 120
 DB 61 PEKNRPLKGRINLVLSRELKPEPPQGAHFLSLDLDALXLTQPELANKVDMVMVIVGGSSV 120
 QY 121 YKEAMNHGHLKLFVTRINQDFESTFPPEIDLEKYLPLPYGVLSDVQBEKGIKYKFE 180
 DB 121 YKEAMNHGHLKLFVTRINQDFESTFPPEIDLEKYLPLPYGVLSDVQBEKGIKYKFE 180
 QY 181 VYEKND 186
 DB 181 VYEKND 186

A:Molecule type: DNA
A:Residues: 1-186 <GEC>
A:Cross-references: EMBL:X58774; NID:G60412; PIDN:CAA41575.1; PID:G60413
A:Experimental source: strain 484-77
C:Superfamily: type I dihydrofolate reductase; type I dihydrofolate reductase homology
C:Keywords: NADP; oxidoreductase
F:4-125/Domain: type I dihydrofolate reductase homology <DPR>
F:31.35,64,70/Binding site: substrate (Asp, Phe, Asn, Arg) #status predicted

Query Match 79.0%; Score 772.5; DB 2; Length 186;
Best Local Similarity 81.3%; Pred. No. 1.5e-60;
Matches 148; Conservative 14; Mismatches 19; Indels 1; Gaps 1;

QY 4 LNCIVAVSQNGIGKNGDLPPFLNENRYFQRMTTSSVEGKONLVIMGKKTWFSIPEK 63
DB 5 LNCIVAVSQNGIGKNGDLPPFLNENRYFQRM-TTSSVKNQNLVIMGKKTWFSIPEK 63

QY 64 NRPLKGRINLVLSRELKPEPPQGAHFLSRSLDALKLTQPELANKVDVWVIVGGSSVYKE 123
DB 64 NRPLKDRINLVLSKLEIIPGAHFLARSLDALKLTQPELVNKNVDMVWVIVGGSSVYKD 123

QY 124 ANNHGCHLKFVTRIMQFESDTFFPEIDLEKYLPPYPGVLSDVQBEKGIRKFEVYE 183
DB 124 ANNYGSHLKFVTRIMQFESDTFFPEIDLEKYLPPYPGVLSDVQBEKGIRKFEVYE 183

QY 184 KN 185
DB 184 KN 185

RESULT 10
RDBEHS
dihydrofolate reductase (EC 1.5.1.3) - saimiriine herpesvirus 1 (strain 488)
C:Species: saimiriine herpesvirus 1
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-2004
C:Accession: E34770
R:Biesinger, B.; Trimble, J.J.; Desrosiers, R.C.; Fleckenstein, B.
Virology 176, 505-514, 1990
A:Title: The divergence between two oncogenic Herpesvirus saimiri strains in a genomic
A:Reference number: A34770; MUID:90266466; PMID:2161148
A:Accession: E34770
A:Molecule type: DNA
A:Residues: 1-213 <BIE>
A:Cross-references: EMBL:M55264; NID:G331005; PIDN:AAA72932.1; PID:G331010
C:Superfamily: Dihydrofolate reductase; type I dihydrofolate reductase homology
C:Keywords: methotrexate resistance; NADP; oxidoreductase; trimethoprim resistance
F:4-125/Domain: type I dihydrofolate reductase homology <DPR>
F:31.35,64,70/Binding site: substrate (Asp, Phe, Asn, Arg) #status predicted

Query Match 78.1%; Score 763.5; DB 1; Length 213;
Best Local Similarity 81.2%; Pred. No. 1.1e-59;
Matches 147; Conservative 13; Mismatches 20; Indels 1; Gaps 1;

QY 4 LNCIVAVSQNGIGKNGDLPPFLNENRYFQRMTTSSVEGKONLVIMGKKTWFSIPEK 63
DB 5 LNCIVAVSQNGIGKNGDLPPFLNENRYFQRM-TTSSVKNQNLVIMGKKTWFSIPEK 63

QY 64 NRPLKGRINLVLSRELKPEPPQGAHFLSRSLDALKLTQPELANKVDVWVIVGGSSVYKE 123
DB 64 NRPLKDRINLVLSKLEIIPGAHFLARSLDALKLTQPELVNKNVDMVWVIVGGSSVYKD 123

QY 124 ANNHGCHLKFVTRIMQFESDTFFPEIDLEKYLPPYPGVLSDVQBEKGIRKFEVYE 183
DB 124 ANNYGSHLKFVTRIMQFESDTFFPEIDLEKYLPPYPGVLSDVQBEKGIRKFEVYE 183

QY 184 K 184
DB 184 K 184

RESULT 11
RDBCHD
dihydrofolate reductase (EC 1.5.1.3) - chicken

C:Species: Gallus gallus (chicken)
C:Date: 31-Jul-1980 #sequence_revision 31-Jul-1980 #text_change 16-Aug-2004
C:Accession: A00390; S66557
R:Kumar, A.A.; Blankenship, D.T.; Kaufman, B.T.; Freisheim, J.H.
Biochemistry 19, 667-678, 1980
A:Title: Primary structure of chicken liver dihydrofolate reductase.
A:Reference number: A00390; MUID:80130564; PMID:6766736
A:Accession: A00390
A:Molecule type: protein
A:Residues: 1-189 <KUM>
A:Cross-references: UNIPROT:P00378
R:Pan, Y.; Ju, M.; Zhou, J.; Tsou, C.
Biochem. J. 315, 97-102, 1996
A:Title: Activation of chicken liver dihydrofolate reductase by urea and guanidine hydr
A:Reference number: S66557; MUID:96207568; PMID:8670138
A:Accession: S66557
A:Molecule type: protein
A:Residues: 19-22;138-140,'Q',158-161 <PAN>
C:Superfamily: Dihydrofolate reductase; type I dihydrofolate reductase homology
C:Keywords: NADP; oxidoreductase
F:3-123/Domain: type I dihydrofolate reductase homology <DPR>
F:30,34,64,70/Binding site: substrate (Glu, Phe, Asn, Arg) #status predicted

Query Match 74.6%; Score 730; DB 1; Length 189;
Best Local Similarity 74.6%; Pred. No. 8e-57;
Matches 138; Conservative 24; Mismatches 23; Indels 0; Gaps 0;

QY 1 VGSINCIIVAVSQNGIGKNGDLPPFLNENRYFQRMTTSSVEGKONLVIMGKKTWFSI 60
DB 1 VRSLSINIVAVSQNGIGKNGDLPPFLNENRYFQRM-TSHVGEKQNAIVIMGKKTWFSI 60

QY 61 PEKNRPLKGRINLVLSRELKPEPPQGAHFLSRSLDALKLTQPELANKVDVWVIVGGSSV 120
DB 61 PEKNRPLKDRINLVLSRELKPEPPQGAHFLSRSLDALKLTQPELANKVDVWVIVGGTAV 120

QY 121 YKAMNHGHLKLFVTRIMQFESDTFFPEIDLEKYLPPYPGVLSDVQBEKGIRKFE 180
DB 121 YKAAEKPINHLFVTRILHEFESDTFFPEIDYKDFKLLTEYPGPVADIQEEDGIQKFE 180

QY 181 VYEKN 185
DB 181 VYOKS 185

RESULT 12
S17984
dihydrofolate reductase (EC 1.5.1.3) - forest day mosquito
C:Species: Aedes albopictus (forest day mosquito)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S17984
R:Shotkoski, F.A.; Fallon, A.M.
Eur. J. Biochem. 201, 157-160, 1991
A:Title: An amplified insect dihydrofolate reductase gene contains a single intron.
A:Reference number: S17984; MUID:92007869; PMID:1915358
A:Accession: S17984
A:Molecule type: DNA
A:Residues: 1-186 <SHO>
A:Cross-references: UNIPROT:P28019; EMBL:X60192; NID:G55555; PIDN:CAA42748.1; PID:G55556
C:Genetics:
A:Introns: 27/2
C:Superfamily: type I dihydrofolate reductase; type I dihydrofolate reductase homology
C:Keywords: NADP; oxidoreductase
F:3-123/Domain: type I dihydrofolate reductase homology <DPR>

Query Match 40.7%; Score 398.5; DB 2; Length 186;
Best Local Similarity 44.5%; Pred. No. 9.7e-28;
Matches 81; Conservative 36; Mismatches 56; Indels 9; Gaps 4;

QY 7 IVAVSQNGIGKNGDLPPFLNENRYFQRM-TTSSVEGKONLVIMGKKTWFSIPEKRP 66
DB 7 IVAVCANGGIGKNGDLPPWR-LQELKYFGRMTKKIQDSGKRNAIVIMGKKTWFSIPEKRP 65

QY 67 LKGRINLVLSRELKPEPPQGAH----FLSRSLDALKLTQPELANKVDVWVIVGGSSVYK 122

Db 66 LPERLNIILTR---DPSANAYSEVWVCTSQEALKKLDEAPLVNENIENWIVGNNAVYK 122
 Qy 123 EAMNHPGHLKLVTRIMQDFSDTFFPRIDLEKYKLLPEYFGVLSDVQEEKGIYKKEVY 182
 Db 123 EAMQSDRCHRIYLTETFECDAPFRITSD-FOLVAKDDVDVPEDIQEENGIOYQYRIY 181
 Qy 183 EK 184
 Db 182 EK 183

RESULT 13
 A53803
 C:Species: Drosophila melanogaster
 C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 16-Aug-2004
 C:Accession: A53803
 R:Haag, H.; Tyshenko, M.G.; Walker, V.K.
 J. Biol. Chem. 269, 15179-15185, 1994
 A:Title: Dihydrofolate reductase of Drosophila. Cloning and expression of a gene with a
 A:Reference number: A53803; MUID:94253079; PMID:8195153
 A:Accession: A53803
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-182 <HAO>
 A:Cross-references: UNIPROT:P17719; GB:U06861; NID:g500629; PIDN:AAA19051.1; PID:g500630
 C:Genetics:
 A:Gene: Dhfr
 A:Cross-references: FlyBase:FBgn0004087
 A:Introns: 27/2
 C:Superfamily: Dihydrofolate reductase; type I dihydrofolate reductase homology
 C:Keywords: NADP; oxidoreductase
 F:3-122/Domain: type I dihydrofolate reductase homology <DFR>

Query Match 40.7%; Score 398; DB 2; Length 182;
 Best Local Similarity 46.0%; Pred. No. 1e-27;
 Matches 86; Conservative 37; Mismatches 48; Indels 16; Gaps 6;
 Qy 5 NCIVAVSQNMIGKNGDLFPWFLRNEFRYFORMTTSSVEGKQNLVIMGKKTWFSIPEKN 64
 Db 5 NLIVAVCNFGIGIRGDLFWR-IKSELKYFSRTKRTSDPTKQNAVVMGRKTYFGVPESK 63
 Qy 65 RLKGRINLVLSRELKEP--PGAHFLSRDLDALKLQEPALANKVDMVWIVGSSVYK 122
 Db 64 RLPLRLNIVLSTLQESDLPGV-LLCPNLETAKLLEE---QNEVENIWIIVGSGVYE 119
 Qy 123 EAMNHPGHLKLVTRIMQDFSDTFFPRIDLEKYKLLPEYFGVLSDVQEEKGIYK 178
 Db 120 EAMASPRCHRLVITQIMQKFCDDTFFPAIPDSFREAVPD----SDMPLGVQEEGIKFE 174
 Qy 179 FEVYEKN 185
 Db 175 YKILEKH 181

RESULT 14
 I73445
 C:Species: Homo sapiens (man)
 C:Date: 02-Aug-1996 #sequence_revision 31-Dec-1996 #text_change 20-Apr-2000
 C:Accession: I73445
 R:Masters, J.N.; Yang, J.K.; Cellini, A.; Attardi, G.
 C: Mol. Biol. 167, 23-36, 1993
 A:Title: A human dihydrofolate reductase pseudogene and its relationship to the multiple
 A:Reference number: 156377; MUID:83241747; PMID:6306253
 A:Accession: I73445
 A:Status: translated from GB/EMBL/DBJ; conceptual translation of pseudogene
 A:Molecule type: mRNA
 A:Residues: 1-97 <NAA>
 A:Cross-references: GB:J00146; NID:g182732; PIDN:AAA52469.1; PID:g553296
 C:Genetics:
 A:Gene: GDB:DHFRP1

A:Cross-references: GDB:I119093
 A:Map position: 18q12.1-18q12.1
 C:Keywords: pseudogene

Query Match 36.6%; Score 358; DB 4; Length 97;
 Best Local Similarity 78.7%; Pred. No. 1.5e-24;
 Matches 70; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Qy 1 VGSINCIVAVSQNMIGKNGDLFPWFLRNEFRYFORMTTSSVEGKQNLVIMGKKTWFSI 60
 Db 2 VSLINCIVAVSQNMIGKNGDLFPWFLRNEFRYFORMTTSSVEGKQNLVIMGKKTWFSI 61
 Qy 61 PEKNRELKGRINLVLSRELKEP--PGAHFL 89
 Db 62 PEKNRELKGRINLVLRDRDHKLHKEINFL 90

RESULT 15
 T19778
 C:hypothetical protein C36B1.7 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T19778
 R:Lennard, N.
 Submitted to the EMBL Data Library, September 1996
 A:Reference number: Z19176
 A:Accession: T19778
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-189 <WIL>
 A:Cross-references: UNIPROT:O93341; EMBL:Z80215; PIDN:CAB02272.1; GSPDB:GN00019; GESP:CG
 A:Experimental source: clone C36B1
 C:Genetics:
 A:Gene: CESP:C36B1.7
 A:Map position: 1
 A:Introns: 45/3; 89/2; 140/2
 C:Superfamily: type I dihydrofolate reductase; type I dihydrofolate reductase hemo

Query Match 32.7%; Score 319.5; DB 2; Length 189;
 Best Local Similarity 36.0%; Pred. No. 8.5e-21;
 Matches 64; Conservative 41; Mismatches 70; Indels 3; Gaps 2;
 Qy 4 LNCIVAVSQNMIGKNGDLFPWFLRNEFRYFORMTTSSVEGKQNLVIMGKKTWFSIPEK 63
 Db 4 MLLIVAMDRAEGGIGKNGVLPWR-IKKDMQYFASVTKNVSDQSKRNVLMGRKWCESIPT 62
 Qy 64 NRPLKGRINLVLSRELKEP--PGAHFLSRDLDALKLQEPALANKVDMVWIVGSSVYKE 123
 Db 63 RRPLAGRLNIVLSROLPAQKSDDYIVVNSLEAAMKLLSEPPFVDSIETIWNITGGAEIYDL 122
 Qy 124 AMNHPGHLKLVTRIMQDFSDTFFPRIDLEKYKLL--PEYFGVLSDVQEEKGIYK 179
 Db 123 ALRENLVDEIHUTRIFKNFEADVHLKSLDFSQKQVQNAEVSSENSEIFEENGLAFEP 180

Search completed: November 19, 2004, 13:52:42
 Job time : 17 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 13:48:23 ; Search time 69 Seconds
(without alignments)

1551.010 Million cell updates/sec

Title: US-10-650-417-7

Perfect score: 978

Sequence: 1 VGSUNCIIVASQNMIGKNG.....SDVQEEKGIKFEVYEKND 186

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	968	99.0	186	1	DYR_HUMAN	P00374 homo sapien
2	968	99.0	187	2	AAH71996	Aah71996 homo sapi
3	965	98.7	187	2	Q61RW8	Q61rw8 homo sapien
4	965	98.7	187	2	AAH70280	Aah70280 homo sapi
5	836	91.6	187	2	Q520D2	Q520d2 rattus norv
6	832	91.2	186	1	DYR_MESAU	P04753 mesocricetu
7	892	91.2	187	2	Q78EE3	Q78ee3 cricetus
8	887	90.7	187	2	Q78EH1	Q78eh1 cricetus
9	880	90.0	186	1	DYR_MOUSE	P00375 mus musculu
10	880	90.0	187	2	BAC27315	Bac27315 mus muscu
11	875	89.5	187	2	Q86XFO	Q86xf0 homo sapien
12	874	89.4	187	2	Q8P419	Q8p419 homo sapien
13	874	89.4	187	2	AAH63379	Aah63379 homo sapi
14	862	88.1	186	1	DYR_PIG	P00377 sus scrofa
15	852	87.1	186	1	DYR_BOVIN	P00376 bos taurus
16	907	82.5	187	1	DYR_SHV21	P09503 saimirine
17	772.5	79.0	186	1	DYR_SHV24	P27421 saimirine
18	765.5	78.4	194	2	Q9DSE3	Q9dse3 saimirine
19	763.5	78.1	213	1	DYR_SHV2C	P22573 saimirine
20	763.5	78.1	213	2	Q778B2	Q778b2 saimirine
21	763.5	78.1	213	2	CAC84296	Cac84296 saimirin
22	730	74.6	189	1	DYR_CHICK	P00378 gallus gall
23	599.5	61.3	188	2	Q9WRU3	Q9wru3 macaca mula
24	599.5	61.3	188	2	Q92M7	Q912m7 macaca mula
25	596	60.9	190	2	Q61Q54	Q61q54 brachydanio
26	596	60.9	190	2	AAH71330	Aah71330 brachydan
27	596	60.9	191	2	Q98TR9	Q98tr9 brachydanio
28	473.5	48.4	210	2	O40919	O40919 human herpe
29	473.5	48.3	210	2	P90486	P90486 human herpe
30	399	40.8	182	1	DYR_DROME	P17119 drosophila
31	398.5	40.7	186	1	DYR_AEDAL	P28019 aedes albop

Q8mtj0 haematobia
Q9u8b8 heliothis v
Q7q0l5 anopheles g
Q6i9g8 homo sapien
Q9jbb0 cricetus
Q8jxv3 heliothis z
Q6wea6 hartmannell
AaQ2617 hartmanne
Q6wea2 hartmannell
Q6wea8 hartmannell
AaQ2615 hartmanne
AaQ2621 hartmanne
Q93341 caenorhabdi
Q6wea4 hartmannell

ALIGNMENTS

RESULT 1

DYR_HUMAN
ID DYR_HUMAN STANDARD; PRT; 186 AA.
AC P00374; Q14130;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Dihydrofolate reductase (EC 1.5.1.3).
GN Name=DHFR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84162075; PubMed=6323448;
RA Chen M.-J., Shimada T., Moulton A.D., Cline A., Humphries R.X.,
Maizel J., Nienhuis A.W.;
RT "The functional human dihydrofolate reductase gene.";
RL J. Biol. Chem. 259:3933-3943(1984).
[2]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=83183667; PubMed=6687716;
RA Masters J.N., Attardi G.;
RT "The nucleotide sequence of the cDNA coding for the human dihydrofolic acid reductase.";
RL Gene 21:59-63(1983).
[3]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=84267838; PubMed=6235374;
RA Yang J.K., Masters J.N., Attardi G.;
RT "Human dihydrofolate reductase gene organization. Extensive conservation of the G + C-rich 5' non-coding sequence and strong intron size divergence from homologous mammalian genes.";
RL J. Mol. Biol. 176:169-187(1984).
[4]
RN
RP SEQUENCE FROM N.A.
TX TISSUE=Eye;
RX MEDLINE=22338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uslin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D., Murty D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Heltan E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."; <http://www.ncbi.nlm.nih.gov/PMCID/PMC10801/>.
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [5]
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=88254806; PubMed=3383852;
 RA Oefner C., D'Arcy A., Winkler F.K.;
 RA "Crystal structure of human dihydrofolate reductase complexed with
 RT folate."; <http://www.ncbi.nlm.nih.gov/PMCID/PMC10801/>.
 RL Eur. J. Biochem. 174:377-385 (1988).
 RN [6]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=91064350; PubMed=2248959;
 RA Davies J.F., Delcamp T.J., Prendergast N.J., Ashford V.A.,
 RA Freisheim J.H., Kraut J.;
 RA "Crystal structures of recombinant human dihydrofolate reductase
 RT complexed with folate and 5-deaza-folate."; <http://www.ncbi.nlm.nih.gov/PMCID/PMC10801/>.
 RL Biochemistry 29:9467-9479 (1990).
 RN [7]
 RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RX MEDLINE=98042281; PubMed=9374868;
 RA Cody V., Galitsky N., Luft J.R., Pangborn W., Blakley R.L.,
 RA Ganjee A.;
 RA "Comparison of two independent crystal structures of human
 RT dihydrofolate reductase ternary complexes reduced with nicotinamide
 adenosine dinucleotide phosphate and the very tight-binding inhibitor
 PT523."; <http://www.ncbi.nlm.nih.gov/PMCID/PMC10801/>.
 RL Biochemistry 36:13897-13903 (1997).
 RN [8]
 RN STRUCTURE BY NMR.
 RX MEDLINE=92118795; PubMed=1731871;
 RA Stockman B.J., Nirmala N.R., Wagner G., Delcamp T.J., Deyarman M.T.,
 RA Freisheim J.H.;
 RA "Sequence-specific 1H and 15N resonance assignments for human
 RT dihydrofolate reductase in solution."; <http://www.ncbi.nlm.nih.gov/PMCID/PMC10801/>.
 RL Biochemistry 31:218-229 (1992).
 CC -1- CATALYTIC ACTIVITY: 5,6,7,8-tetrahydrofolate + NADPH(+) = 7,8-
 CC dihydrofolate + NADPH.
 CC -1- PATHWAY: Essential step for de novo glycine and purine synthesis,
 CC DNA precursor synthesis, and for the conversion of dUMP to dTMP.
 CC -1- SIMILARITY: Belongs to the dihydrofolate reductase family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL: J00140; AA58485.1; -;
 DR EMBL: V00507; CA23765.1; -;
 DR EMBL: J00139; AA58484.1; -;
 DR EMBL: X01612; AA58484.1; JOINED.
 DR EMBL: X01613; AA58484.1; JOINED.
 DR EMBL: J00138; AA58484.1; JOINED.
 DR EMBL: X01614; AA58484.1; JOINED.
 DR EMBL: X00855; CA225409.1; -;
 DR EMBL: X00856; CA225409.1; JOINED.
 DR EMBL: X00857; CA225409.1; JOINED.
 DR EMBL: X00858; CA225409.1; JOINED.
 DR EMBL: X00859; CA225409.1; JOINED.
 DR EMBL: BC000192; AAH00192.1; -;
 DR EMBL: BC003584; AAH03584.2; -;
 DR PIR: A22551; RDHUF.
 DR PDB: 1BDF; X-ray; A=1-186.
 DR PDB: 1DLR; X-ray; @=1-186.
 DR PDB: 1DLS; X-ray; @=1-186.
 DR PDB: 1DRF; X-ray; @=1-186.
 DR PDB: 1HFP; X-ray; @=1-186.

DR PDB: 1HFO; X-ray; @=1-186.
 DR PDB: 1HFR; X-ray; @=1-186.
 DR PDB: 1KMS; X-ray; A=1-186.
 DR PDB: 1KVV; X-ray; A=1-186.
 DR PDB: 1MVS; X-ray; A=1-186.
 DR PDB: 1MVT; X-ray; A=1-186.
 DR PDB: 1OHJ; X-ray; @=1-186.
 DR PDB: 1OHK; X-ray; @=1-186.
 DR PDB: 1PD8; X-ray; A=1-186.
 DR PDB: 1PD9; X-ray; A=1-186.
 DR PDB: 1PDB; X-ray; A=1-186.
 DR PDB: 2DHF; X-ray; A/B=1-186.
 DR HSC-2DPAGE; P00374; HUMAN.
 DR MIM; 126060; -;
 DR GO: GO:0004146; F: dihydrofolate reductase activity; NAS.
 DR GO: GO:0006545; P: glycine biosynthesis; NAS.
 DR GO: GO:0009165; P: nucleotide biosynthesis; NAS.
 DR InterPro: IPR001796; DHFR.
 DR Pfam: PF00186; Dihfolate_red; 1.
 DR PRINTS; PR0070; DHFR.
 DR PROSITE; PS00075; DHFR; 1.
 KW 3D-structure; NADP; One-carbon metabolism; Oxidoreductase.
 FT INIT MET 0
 FT STRAND 4 10
 FT TURN 12 13
 FT STRAND 15 18
 FT TURN 19 20
 FT STRAND 21 21
 FT HELIX 28 39
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 FT HELIX 62 64
 FT TURN 68 69
 FT STRAND 71 75
 FT TURN 84 85
 FT STRAND 88 90
 FT HELIX 93 100
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 FT TURN 103 108
 FT STRAND 109 114
 FT HELIX 118 125
 FT TURN 126 126
 FT STRAND 131 138
 FT STRAND 146 147
 FT TURN 153 155
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 FT TURN 163 164
 FT STRAND 170 172
 FT TURN 173 174
 FT STRAND 175 184
 SQ SEQUENCE 186 AA; 21321 MW; EBB9E6A3ECA8CEDB CRC64;
 Query Match 99.0%; Score 968; DB 1; Length 186;
 Best Local Similarity 99.5%; Pred. No. 8.7e-78;
 Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VGLACIVAVSONMGIGKNGDLFWPFLRNEFRYFORMTTTSVEGKQNLVIMGKKTWFSI 60
 DB 1 VGLACIVAVSONMGIGKNGDLFWPFLRNEFRYFORMTTTSVEGKQNLVIMGKKTWFSI 60
 QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDALKLTPQELANKVDMVWIVGGSSV 120
 DB 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDALKLTPQELANKVDMVWIVGGSSV 120
 QY 121 YXEAMNHPGHLKLVTRIMQDFESDTFFPEIDLEKYKLLPYPGVLSVQBEKGKIKYKFE 180
 DB 121 YXEAMNHPGHLKLVTRIMQDFESDTFFPEIDLEKYKLLPYPGVLSVQBEKGKIKYKFE 180
 QY 181 VYEKND 186
 DB 181 VYEKND 186


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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Dhhydrofolate reductase.
GN Name=DHFR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;
[1]
RN SEQUENCE FROM N.A.
RP
RC TISSUE=Pooled;
RX MEDLINE=22388257; PubMed=12477932;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapellato M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Besak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyak S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywanski M.I., Skalska U., Smailus D.Z., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RP
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP
RC TISSUE=Pooled;
RA Srausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC070280; AAH70280.1; -
DR InterPro; IPR001796; DHFR.
DR Pfam; PF00186; DHFR.1; 1.
DR PRINTS; PR00070; DHFR.
DR PROSITE; PS00075; DHFR; 1.
SQ SEQUENCE 187 AA; 21467 MW; BBD2F1F03522FB94 CRC64;

Query Match 98.7%; Score 965; DB 2; Length 187;
Best Local Similarity 98.9%; Pred. No. 1.6e-77;
Matches 184; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 1 VGSINCIIVASQNGTGKNGDLPPWPLRNFRFQRTTTSSVEGKNLVIMGKKTWFSI 60
Db 2 VGSINCIIVASQNGTGKNGDLPPWPLRNFRFQRTTTSSVEGKNLVIMGKKTWFSI 61

Cy 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLITEQELANKVDWVIVGSSV 120
Db 62 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLITEQELANKVDLVIVGSSV 121

Cy 121 YKEAMNHPGHLKLVFVTRIMODFSDFTPFPIDILEKYKLLPEYPGVLSGVQBEKGIKYKFE 180
Db 122 YKEAMNHPGHLKLVFVTRIMODFSDFTPFPIDILEKYKLLPEYPGVLSGVQBEKGIKYKFE 181

Cy 181 VYEKND 186
Db 182 VYEKND 187

RESULT 4
AAH70280 PRELIMINARY; PRT; 187 AA.
AC AAH70280;
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.

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RESULT 2
AAH71996
ID AAH71996 PRELIMINARY; PRT; 187 AA.
AC AAH71996;
DT 01-JUN-2004 (TREMBlrel. 27, Created)
DT 01-JUN-2004 (TREMBlrel. 27, Last sequence update)
DT 01-JUN-2004 (TREMBlrel. 27, Last annotation update)
DE Dihydrofolate reductase.
GN DHFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.J., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RT TISSUE=Eye;
RX Strausberg R.;
RL Submitted (JUN-2004) to the ENBL/GenBank/DBJ databases.
DR ENBL; BC071996; AAH71996.1; -.
SQ SEQUENCE 187 AA; 21453 MW; EBDF3D1EC7B1566 CRC64;

Query Match 99.0%; Score 968; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 8,78-78;
Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Qy * 1 VGSLLNCIVAVSQNMGIKNGDLPPFLRNEFRYFQRMTTTSSVEGKQNLVIMGKKTWFSI 60
Db 2 VGSLLNCIVAVSQNMGIKNGDLPPFLRNEFRYFQRMTTTSSVEGKQNLVIMGKKTWFSI 61

Qy 61 PEKNPLKGRINLVLSRELKEPPOGAHLRSLLDDALKL TEQELANKYMDVMWVGGSV 120
Db 62 PEKNPLKGRINLVLSRELKEPPOGAHLRSLLDDALKL TEQELANKYMDVMWVGGSV 121

Qy 121 YKEAMNHGHGLKFLVTRIMQDFESDTFPPEIDLEKYKLLPEYFGVLSDVQEEKGIKYFE 180
Db 122 YKEAMNHGHGLKFLVTRIMQDFESDTFPPEIDLEKYKLLPEYFGVLSDVQEEKGIKYFE 181

Qy 181 VYEKND 186
Db 182 VYEKND 187

RESULT 3
Q6IRW8 PRELIMINARY; PRT; 187 AA.
ID Q6IRW8
AC Q6IRW8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)

```

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pooled;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schenker C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RE Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pooled;
 RX Strausberg R.;
 RE Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC070280; AAH70280.1; --
 KW Hypothetical protein.
 SQ SEQUENCE 187 AA; 21467 MW; EBD21F03522FB94 CRC64;

Query Match 98.7%; Score 965; DB 2; Length 187;
 Best Local Similarity 98.9%; Pred. No. 1.6e-77;
 Matches 184; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGLNCIVAVSQNMIGKNGDLPWPLNFRYQRMITTSVEGKQNLVIMGKTWFSI 60
 DB 2 VGLNCIVAVSQNMIGKNGDLPWPLNFRYQRMITTSVEGKQNLVIMGKTWFSI 61
 QY 61 PEKNRPLKGRINLVLSRELKPPQGAHFLSLRSLDALKLTPQELANKVDMVWVGGSSV 120
 DB 62 PEKNRPLKGRINLVLSRELKPPQGAHFLSLRSLDALKLTPQELANKVDMVWVGGSSV 121
 QY 121 YKEAMNHGHLKLFVTRIMQDPESDTFFPEIDLEKYLPPYGVLSVQVEKGKIKYKFE 180
 DB 122 YKEAMNHGHLKLFVTRIMQDPESDTFFPEIDLEKYLPPYGVLSVQVEKGKIKYKFE 181
 QY 181 VYEKND 186
 DB 182 VYEKND 187

RESULT 5
 Q920D2 PRELIMINARY; PRT; 187 AA.
 AC Q920D2;
 DT 01-DEC-2001 (TREMELrel. 19, Created)
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Dihydrofolate reductase.
 GN Name=Dhfr;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=21393659; PubMed=11502523;
 RA Wang Y., Bruenn J.A., Queener S.F., Cody V.;
 RT "Isolation of rat dihydrofolate reductase gene and characterization of
 RT recombinant enzyme.";
 RL Antimicrob. Agents Chemother. 45:2517-2523(2001).
 DR EMBL; AF318150; AAL11500.1; --
 DR HSSP; P00374; 1KMS.
 DR GO: GO:0004146; F.dihydrofolate reductase activity; IEA.
 DR GO: GO:0005454; P.glycine biosynthesis; IEA.
 DR GO: GO:0009165; P.nucleotide biosynthesis; IEA.
 DR InterPro; IPR001796; DHFR.
 DR Pfam; PF00186; DHFR_1; 1.
 DR PRINTS; PR00070; DHFR.
 DR PROSITE; PS00075; DHFR; 1.
 SQ SEQUENCE 187 AA; 21638 MW; FE1DB4F3515F9B26 CRC64;

Query Match 91.6%; Score 896; DB 2; Length 187;
 Best Local Similarity 89.8%; Pred. No. 2.1e-71;
 Matches 157; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 1 VGLNCIVAVSQNMIGKNGDLPWPLNFRYQRMITTSVEGKQNLVIMGKTWFSI 60
 DB 2 VPLNCIVAVSQNMIGKNGDLPWPLNFRYQRMITTSVEGKQNLVIMGKTWFSI 61
 QY 61 PEKNRPLKGRINLVLSRELKPPQGAHFLSLRSLDALKLTPQELANKVDMVWVGGSSV 120
 DB 62 PEKNRPLKGRINLVLSRELKPPQGAHFLSLRSLDALKLTPQELANKVDMVWVGGSSV 121
 QY 121 YKEAMNHGHLKLFVTRIMQDPESDTFFPEIDLEKYLPPYGVLSVQVEKGKIKYKFE 180
 DB 122 YKEAMNHGHLKLFVTRIMQDPESDTFFPEIDLEKYLPPYGVLSVQVEKGKIKYKFE 181
 QY 181 VYEKND 186
 DB 182 VYEKND 187

RESULT 6
 Dyr MESAU STANDARD; PRT; 186 AA.
 ID Dyr MESAU STANDARD; PRT; 186 AA.
 AC P04753;
 DT 13-AUG-1987 (rel. 05, Created)
 DT 01-FEB-1996 (rel. 33, Last sequence update)
 DT 05-JUL-2004 (rel. 44, Last annotation update)
 DE Dihydrofolate reductase (EC 1.5.1.3).
 GN Name=DHFR;
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88115326; PubMed=3339001;
 RA Melera P.W., Davide J.P., Oen H.;
 RT "Antifolate-resistant Chinese hamster cells. Molecular basis for the
 RT biochemical and structural heterogeneity among dihydrofolate
 RT reductases produced by drug-sensitive and drug-resistant cell lines.";
 RL J. Biol. Chem. 263:1978-1990(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84141864; PubMed=6366511;
 RA Melera P.W., Davide J.P., Hession C.A., Scotto K.W.;
 RT "Phenotypic expression in Escherichia coli and nucleotide sequence of
 RT two Chinese hamster lung cell cDNAs encoding different dihydrofolate
 RT reductases.";
 RL Mol. Cell. Biol. 4:38-48(1984).
 RN [3]
 RP ERRATUM.
 RA Melera P.W., Davide J.P., Hession C.A., Scotto K.W.;
 RL Mol. Cell. Biol. 4:1001-1001(1984).

CC -!- CATALYTIC ACTIVITY: 5,6,7,8-tetrahydrofolate + NADP(+) = 7,8-dihydrofolate + NADPH.
 CC -!- PATHWAY: Essential step for de novo glycine and purine synthesis, DNA precursor synthesis, and for the conversion of dUMP to dTMP.
 CC -!- POLYMORPHISM: The sequence shown is that of A3-35. The two clones A3-35 and MQ19-97 represent allelic forms. They differ in their drug sensitivities, possibly because of the difference at position 22.
 CC -!- MISCELLANEOUS: Overexpression of the dihydrofolate gene (generally involving gene amplification) results in resistance to the antitumor antifolate drugs methotrexate (MTX) and methasquin.
 CC -!- MISCELLANEOUS: Cell line DC-3F/A3 produces 90% of its dihydrofolate reductase in the 21k pI 6.5 form.
 CC -!- MISCELLANEOUS: Cell line DC-3F/MQ19 produces 90% of its dihydrofolate reductase in the 20k pI 6.7 form (DHFR97).
 CC -!- SIMILARITY: Belongs to the dihydrofolate reductase family.

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DR EMBL; X01164; AAA36974.1; -.
 DR EMBL; X01165; AAA36976.1; -.
 DR EMBL; M19869; AAA36970.1; -.
 DR HSP; P00374; 1KX5.
 DR InterPro; IPR001796; DHFR.
 DR Pfam; PF00186; Dihfolate_red; 1.
 DR PRINTS; PR00070; DHFR.
 DR PROSITE; PS00075; DHFR; 1.
 DR Method:reductase resistance; NADP; One-carbon metabolism; Oxidoreductase; Polyomorphism.
 FT INIT_MET 0 0
 FT SITE 7 9 INVOLVED IN MTX BINDING (BY SIMILARITY).
 FT SITE 22 22 INVOLVED IN MTX BINDING (BY SIMILARITY).
 FT SITE 30 31 INVOLVED IN MTX BINDING (BY SIMILARITY).
 FT SITE 34 34 INVOLVED IN MTX BINDING (BY SIMILARITY).
 FT SITE 36 36 INVOLVED IN MTX BINDING (BY SIMILARITY).
 FT SITE 59 69 INVOLVED IN MTX BINDING (BY SIMILARITY).
 FT SITE 115 115 INVOLVED IN MTX BINDING (BY SIMILARITY).
 FT SITE 136 136 INVOLVED IN MTX BINDING (BY SIMILARITY).
 FT SITE 22 22 F -> L (in MQ19-97).
 FT VARIANT 95 95 D -> N (in MQ19-97).
 SQ SEQUENCE 186 AA; 21529 MW; A9795E1A6DC51D4E CRC64;

Query Match 91.2%; Score 892; DB 1; Length 186;
 Best Local Similarity 91.3%; Pred. No. 4.8e-71;
 Matches 168; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
 QY 1 VGSNCIVAVSQNMIGKNGKQDLPWPLRNEFRYFQRMFTTSSVEGKQNLVINGKKTWFSI 60
 Db 1 VRPLNCIVAVSQNMIGKNGKQDLPWPLRNEFRYFQRMFTTSSVEGKQNLVINGKKTWFSI 60
 QY 61 PEKRNPLKGRINVLVSRELKEPPQGAHFLSLDDALKLTPQELANKVDMVWIVGSSV 120
 Db 61 PEKRNPLKGRINVLVSRELKEPPQGAHFLSLDDALKLTPQELANKVDMVWIVGSSV 120
 QY 121 YKEAMNHPGHLKLFVTRIMQFESDTFFPEIDLEKYLPPYGVLSVQVEKGIKYKFE 180
 Db 121 YKEAMNHPGHLKLFVTRIMQFESDTFFPEIDLEKYLPPYGVLSVQVEKGIKYKFE 180
 QY 181 VYEK 184
 Db 181 VYEK 184

RESULT 7
 Q78EE3 PRELIMINARY; PRT; 187 AA.
 ID Q78EE3
 AC Q78EE3;

DT 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 OS Cricetulus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.
 OX NCBI_TaxID=10031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90243717; PubMed=2335526;
 RA Dicker A.P., Volkenandt M., Schweitzer B.I., Banerjee D., Bertino J.R.;
 RT "Identification and characterization of a mutation in the dihydrofolate reductase gene from the methotrexate-resistant Chinese hamster ovary cell line Pro-3 MTX-R111.";
 RL J. Biol. Chem. 265:8317-8321(1990).
 DR EMBL; M37124; AAA36971.1; -.
 DR GO; GO:0004146; Fdihydrofolate reductase activity; IEA.
 DR GO; GO:0016491; Foxidoreductase activity; IEA.
 DR InterPro; IPR001796; DHFR.
 DR Pfam; PF00186; DHFR_1; 1.
 DR PRINTS; PR00070; DHFR.
 DR PROSITE; PS00075; DHFR; 1.
 DR Oxidoreductase.
 SQ SEQUENCE 187 AA; 21660 MW; A91F85A74658C6F3 CRC64;

Query Match 91.2%; Score 892; DB 2; Length 187;
 Best Local Similarity 91.3%; Pred. No. 4.8e-71;
 Matches 168; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
 QY 1 VGSNCIVAVSQNMIGKNGKQDLPWPLRNEFRYFQRMFTTSSVEGKQNLVINGKKTWFSI 60
 Db 2 VRPLNCIVAVSQNMIGKNGKQDLPWPLRNEFRYFQRMFTTSSVEGKQNLVINGKKTWFSI 61
 QY 61 PEKRNPLKGRINVLVSRELKEPPQGAHFLSLDDALKLTPQELANKVDMVWIVGSSV 120
 Db 62 PEKRNPLKGRINVLVSRELKEPPQGAHFLSLDDALKLTPQELANKVDMVWIVGSSV 121
 QY 121 YKEAMNHPGHLKLFVTRIMQFESDTFFPEIDLEKYLPPYGVLSVQVEKGIKYKFE 180
 Db 122 YKEAMNHPGHLKLFVTRIMQFESDTFFPEIDLEKYLPPYGVLSVQVEKGIKYKFE 181
 QY 181 VYEK 184
 Db 182 VYEK 185

RESULT 8

Q78EH1 PRELIMINARY; PRT; 187 AA.
 ID Q78EH1
 AC Q78EH1
 DT 05-JUL-2004 (TEMBLrel. 27, Created)
 DE 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE Dihydrofolate reductase.
 OS Cricetulus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.
 OX NCBI_TaxID=10031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Yu M., Melena P.W.;
 RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L15311; AAA36972.1; -.
 DR InterPro; IPR001796; DHFR.
 DR Pfam; PF00186; DHFR_1; 1.
 DR PRINTS; PR00070; DHFR.
 DR PROSITE; PS00075; DHFR; 1.
 SQ SEQUENCE 187 AA; 21659 MW; A71F65ADECS26659 CRC64;

Query Match 90.7%; Score 887; DB 2; Length 187;
Best Local Similarity 90.8%; Pred. No. 1.3e-70;
Matches 167; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

1 VGSLLCIIVAVSONMGIGKNGDLPPFLNRNFRYQFQWTTTSSVEGKQNLVIMGKTKWFSI 60
2 VRLPLNCIVAVSONMGIGKNGDPPFLNRNFRYQFQWTTTSSVEGKQNLVIMGKTKWFSI 61
61 PEKNRPLKGRINLVLSRELKEPPQCAHFLRSRLDALKLTEOPELANKYDVMWVIYGGSSV 120
62 PEKNRPLKDRINLVLSRELKEPPQCAHFLRSRLDALKLIEQPELADKVDVMWVIYGGSSV 121
121 YKEAMNHPGHLKLFVTRIMQDFESDTPFPIDLEKYKLLPEYPGVLSVQBEKGIKPKFE 180
122 YKEAMNQPGLRLFVTRIMQDFESDTPFPIDLEKYKLLPEYPGVLSVQBEKGIKPKFE 181
181 VYEK 184
182 VYEK 185

RESULT 9
R_MOUSE STANDARD; PRT: 186 AA.
DYR_MOUSE P00375; P70693; Q61485; Q61487; Q61579;
21-JUL-1986 (Rel. 01, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Dihydrofolate reductase (EC 1.5.1.3).
Name=Dhfr;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE.
TISSUE=Lymphoma;
MEDLINE=79109591; PubMed=762074;
Stone D., Paterson S.J., Raper J.H., Phillips A.W.;
"The amino acid sequence of dihydrofolate reductase from the mouse
lymphoma L1210.";
J. Biol. Chem. 254:480-488(1979).
[2]
SEQUENCE FROM N.A.
MEDLINE=82213979; PubMed=6282858;
Grouse G.F., Simonsen C.C., McEwan R.N., Schimke R.T.;
"Structure of amplified normal and variant dihydrofolate reductase
genes in mouse sarcoma S180 cells.";
J. Biol. Chem. 257:7887-7897(1982).
[3]
SEQUENCE FROM N.A.
MEDLINE=83195084; PubMed=6573667;
Simonsen C.C., Levinson A.D.;
"Isolation and expression of an altered mouse dihydrofolate reductase
cDNA.";
Proc. Natl. Acad. Sci. U.S.A. 80:2495-2499(1983).
[4]
SEQUENCE FROM N.A.
MEDLINE=91088280; PubMed=2263462;
McIvor R.S., Simonsen C.C.;
"Isolation and characterization of a variant dihydrofolate reductase
cDNA from methotrexate-resistant murine L5178Y cells.";
Nucleic Acids Res. 18:7025-7032(1990).
[5]
SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Mammary gland;
MEDLINE=22388287; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko I., Marusina K., Farmer A.A., Rubin G.M., Hong I.,
Draetta G.F., Lander E.S., Zeng K., White O., Holt A.D., Adams E.R.,
Blumenfeld B., Bork P., Botstein D., Brown J., Bussey T.J., Fink J.L.,
Fitzpatrick G.B., Fulton R.S., Gage F.H., Gagliardi J., Gonsky R.,
Hawthorne J., Heuvelink A.E., Johnson R.E., Johnson V., Jones R.,
Kane M.P., Kent J., Kiziltepe A., Kobayashi M., Kohno T., Kolchak
W., Kornberg J.R., Kornberg M., Krawetz M., Krawetz N., Krawetz P.,
Krawetz T., Krawetz W., Krawetz X., Krawetz Y., Krawetz Z., Krawetz
AA, Krawetz AB, Krawetz AC, Krawetz AD, Krawetz AE, Krawetz AF, Krawetz
AG, Krawetz AH, Krawetz AI, Krawetz AJ, Krawetz AK, Krawetz AL, Krawetz
AM, Krawetz AN, Krawetz AO, Krawetz AP, Krawetz AQ, Krawetz AR, Krawetz
AS, Krawetz AT, Krawetz AU, Krawetz AV, Krawetz AW, Krawetz AX, Krawetz
AY, Krawetz AZ, Krawetz BA, Krawetz BB, Krawetz BC, Krawetz BD, Krawetz
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BK, Krawetz BL, Krawetz BM, Krawetz BN, Krawetz BO, Krawetz BP, Krawetz
BQ, Krawetz BR, Krawetz BS, Krawetz BT, Krawetz BU, Krawetz BV, Krawetz
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CC, Krawetz CD, Krawetz CE, Krawetz CF, Krawetz CG, Krawetz CH, Krawetz
CI, Krawetz CJ, Krawetz CK, Krawetz CL, Krawetz CM, Krawetz CN, Krawetz
CO, Krawetz CP, Krawetz CQ, Krawetz CR, Krawetz CS, Krawetz CT, Krawetz
CU, Krawetz CV, Krawetz CW, Krawetz CX, Krawetz CY, Krawetz CZ, Krawetz
DA, Krawetz DB, Krawetz DC, Krawetz DD, Krawetz DE, Krawetz DF, Krawetz
DG, Krawetz DH, Krawetz DI, Krawetz DJ, Krawetz DK, Krawetz DL, Krawetz
DM, Krawetz DN, Krawetz DO, Krawetz DP, Krawetz DQ, Krawetz DR, Krawetz
DS, Krawetz DT, Krawetz DU, Krawetz DV, Krawetz DW, Krawetz DX, Krawetz
DY, Krawetz DZ, Krawetz EA, Krawetz EB, Krawetz EC, Krawetz ED, Krawetz
EE, Krawetz EF, Krawetz EG, Krawetz EH, Krawetz EI, Krawetz EJ, Krawetz
EK, Krawetz EL, Krawetz EM, Krawetz EN, Krawetz EO, Krawetz EP, Krawetz
EQ, Krawetz ER, Krawetz ES, Krawetz ET, Krawetz EU, Krawetz EV, Krawetz
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FC, Krawetz FD, Krawetz FE, Krawetz FF, Krawetz FG, Krawetz FH, Krawetz
FI, Krawetz FJ, Krawetz FK, Krawetz FL, Krawetz FM, Krawetz FN, Krawetz
FO, Krawetz FP, Krawetz FQ, Krawetz FR, Krawetz FS, Krawetz FT, Krawetz
FU, Krawetz FV, Krawetz FW, Krawetz FX, Krawetz FY, Krawetz FZ, Krawetz
GA, Krawetz GB, Krawetz GC, Krawetz GD, Krawetz GE, Krawetz GF, Krawetz
GG, Krawetz GH, Krawetz GI, Krawetz GJ, Krawetz GK, Krawetz GL, Krawetz
GM, Krawetz GN, Krawetz GO, Krawetz GP, Krawetz GQ, Krawetz GR, Krawetz
GS, Krawetz GT, Krawetz GU, Krawetz GV, Krawetz GW, Krawetz GX, Krawetz
GY, Krawetz GZ, Krawetz HA, Krawetz HB, Krawetz HC, Krawetz HD, Krawetz
HE, Krawetz HF, Krawetz HG, Krawetz HH, Krawetz HI, Krawetz HJ, Krawetz
HK, Krawetz HL, Krawetz HM, Krawetz HN, Krawetz HO, Krawetz HP, Krawetz
HQ, Krawetz HR, Krawetz HS, Krawetz HT, Krawetz HU, Krawetz HV, Krawetz
HW, Krawetz HX, Krawetz HY, Krawetz HZ, Krawetz IA, Krawetz IB, Krawetz
IC, Krawetz ID, Krawetz IE, Krawetz IF, Krawetz IG, Krawetz IH, Krawetz
II, Krawetz IJ, Krawetz IK, Krawetz IL, Krawetz IM, Krawetz IN, Krawetz
IO, Krawetz IP, Krawetz IQ, Krawetz IR, Krawetz IS, Krawetz IT, Krawetz
IU, Krawetz IV, Krawetz IW, Krawetz IX, Krawetz IY, Krawetz IZ, Krawetz
JA, Krawetz JB, Krawetz JC, Krawetz JD, Krawetz JE, Krawetz JF, Krawetz
JG, Krawetz JH, Krawetz JI, Krawetz JJ, Krawetz JK, Krawetz JL, Krawetz
JM, Krawetz JN, Krawetz JO, Krawetz JP, Krawetz JQ, Krawetz JR, Krawetz
JS, Krawetz JT, Krawetz JU, Krawetz JV, Krawetz JW, Krawetz JX, Krawetz
JY, Krawetz JZ, Krawetz KA, Krawetz KB, Krawetz KC, Krawetz KD, Krawetz
KE, Krawetz KF, Krawetz KG, Krawetz KH, Krawetz KI, Krawetz KJ, Krawetz
KK, Krawetz KL, Krawetz KM, Krawetz KN, Krawetz KO, Krawetz KP, Krawetz
KQ, Krawetz KR, Krawetz KS, Krawetz KT, Krawetz KU, Krawetz KV, Krawetz
KW, Krawetz KX, Krawetz KY, Krawetz KZ, Krawetz LA, Krawetz LB, Krawetz
LC, Krawetz LD, Krawetz LE, Krawetz LF, Krawetz LG, Krawetz LH, Krawetz
LI, Krawetz LJ, Krawetz LK, Krawetz LL, Krawetz LM, Krawetz LN, Krawetz
LO, Krawetz LP, Krawetz LQ, Krawetz LR, Krawetz LS, Krawetz LT, Krawetz
LU, Krawetz LV, Krawetz LW, Krawetz LX, Krawetz LY, Krawetz LZ, Krawetz
MA, Krawetz MB, Krawetz MC, Krawetz MD, Krawetz ME, Krawetz MF, Krawetz
MG, Krawetz MH, Krawetz MI, Krawetz MJ, Krawetz MK, Krawetz ML, Krawetz
MM, Krawetz MN, Krawetz MO, Krawetz MP, Krawetz MQ, Krawetz MR, Krawetz
MS, Krawetz MT, Krawetz MU, Krawetz MV, Krawetz MW, Krawetz MX, Krawetz
MY, Krawetz MZ, Krawetz NA, Krawetz NB, Krawetz NC, Krawetz ND, Krawetz
NE, Krawetz NF, Krawetz NG, Krawetz NH, Krawetz NI, Krawetz NJ, Krawetz
NK, Krawetz NL, Krawetz NM, Krawetz NN, Krawetz NO, Krawetz NP, Krawetz
NQ, Krawetz NR, Krawetz NS, Krawetz NT, Krawetz NU, Krawetz NV, Krawetz
NW, Krawetz NX, Krawetz NY, Krawetz NZ, Krawetz OA, Krawetz OB, Krawetz
OC, Krawetz OD, Krawetz OE, Krawetz OF, Krawetz OG, Krawetz OH, Krawetz
OI, Krawetz OJ, Krawetz OK, Krawetz OL, Krawetz OM, Krawetz ON, Krawetz
OO, Krawetz OP, Krawetz OQ, Krawetz OR, Krawetz OS, Krawetz OT, Krawetz
OU, Krawetz OV, Krawetz OW, Krawetz OX, Krawetz OY, Krawetz OZ, Krawetz
PA, Krawetz PB, Krawetz PC, Krawetz PD, Krawetz PE, Krawetz PF, Krawetz
PG, Krawetz PH, Krawetz PI, Krawetz PJ, Krawetz PK, Krawetz PL, Krawetz
PM, Krawetz PN, Krawetz PO, Krawetz PP, Krawetz PQ, Krawetz PR, Krawetz
PS, Krawetz PT, Krawetz PU, Krawetz PV, Krawetz PW, Krawetz PX, Krawetz
PY, Krawetz PZ, Krawetz QA, Krawetz QB, Krawetz QC, Krawetz QD, Krawetz
QE, Krawetz QF, Krawetz QG, Krawetz QH, Krawetz QI, Krawetz QJ, Krawetz
QK, Krawetz QL, Krawetz QM, Krawetz QN, Krawetz QO, Krawetz QP, Krawetz
QQ, Krawetz QR, Krawetz QS, Krawetz QT, Krawetz QU, Krawetz QV, Krawetz
QW, Krawetz QX, Krawetz QY, Krawetz QZ, Krawetz RA, Krawetz RB, Krawetz
RC, Krawetz RD, Krawetz RE, Krawetz RF, Krawetz RG, Krawetz RH, Krawetz
RI, Krawetz RJ, Krawetz RK, Krawetz RL, Krawetz RM, Krawetz RN, Krawetz
RO, Krawetz RP, Krawetz RQ, Krawetz RR, Krawetz RS, Krawetz RT, Krawetz
RU, Krawetz RV, Krawetz RW, Krawetz RX, Krawetz RY, Krawetz RZ, Krawetz
SA, Krawetz SB, Krawetz SC, Krawetz SD, Krawetz SE, Krawetz SF, Krawetz
SG, Krawetz SH, Krawetz SI, Krawetz SJ, Krawetz SK, K

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DR PIR; S13096; RDMSD.
DR HSSP; P00374; IONS.
DR MGD; MG194890; Dhfr.
DR InterPro; IPR001796; DHFR.
DR Pfam; PF00186; Dihydrofolate_red; 1.
DR PRINTS; PR00070; DHFR.
DR PROSITE; PS00075; DHFR; 1.
KW Direct protein sequencing; NADP; One-carbon metabolism;
KW Oxidoreductase.
FT INIT_MET 0
FT VARIANT 22 22
FT VARIANT 31 31
FT CONFLICT 3 3
FT CONFLICT 13 13
FT CONFLICT 122 122
FT CONFLICT 123 123
FT CONFLICT 127 127
FT CONFLICT 173 173
SQ SEQUENCE 186 AA; 21475 MW; 47C82AE2AC0CA21 CRC64;
Query Match 90.0%; Score 880; DB 1; Length 186;
Best Local Similarity 89.2%; Pred. No. 5.6e-70;
Matches 166; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
QY 1 VGSNCIVAVSONMGIGKNGDLPWPFRLNRPYFQRMTTSSVEGKQNLVIMGKKTWFSI 60
DB 1 VRPLNCIVAVSONMGIGKNGDLPWPFRLNRPYFQRMTTSSVEGKQNLVIMGKKTWFSI 60
QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDALKLTEQPELANKVDMMVIVGSSV 120
DB 61 PEKNRPLKDRINIVLSRELKEPPRGAHFLAKSLDLDALRLTEQPELANKVDMMVIVGSSV 120
QY 121 YKEAMNHCHLKLFTVTRIMQDFESDTFFPIDLEKYLLPEYGVLSVQSEKGIKYKPE 180
DB 121 YQEAAMNQGHRLKFLVTRIMQDFESDTFFPIDLGKYLPEYGVLSVQSEKGIKYKPE 180
QY 181 VYEKND 186
DB 181 VYEKND 186
RESULT 10
BAC27315 PRELIMINARY; PRT; 187 AA.
AC BAC27315;
DT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DE 13 days embryo forelimb cDNA, RIKEN full-length enriched library,
DE clone:5930436E06 product:DIHYDROFOLATE REDUCTASE, full insert
DE sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognath.; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Forelimb;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Forelimb;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
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[3]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Forelimb;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[4]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Forelimb;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Forelimb;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Hirozane T.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Forelimb;
RX MEDLINE=20530913; PubMed=11076861;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK031241; BAC27315.1;
SQ SEQUENCE 187 AA; 21606 MW; 47AEF15F879B119C CRC64;
Query Match 90.0%; Score 880; DB 2; Length 187;
Best Local Similarity 89.2%; Pred. No. 5.6e-70;
Matches 166; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
QY 1 VGSNCIVAVSONMGIGKNGDLPWPFRLNRPYFQRMTTSSVEGKQNLVIMGKKTWFSI 60
DB 2 VRPLNCIVAVSONMGIGKNGDLPWPFRLNRPYFQRMTTSSVEGKQNLVIMGKKTWFSI 61
QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDALKLTEQPELANKVDMMVIVGSSV 120
DB 62 PEKNRPLKDRINIVLSRELKEPPRGAHFLAKSLDLDALRLTEQPELANKVDMMVIVGSSV 121
QY 121 YKEAMNHCHLKLFTVTRIMQDFESDTFFPIDLEKYLLPEYGVLSVQSEKGIKYKPE 180
DB 122 YQEAAMNQGHRLKFLVTRIMQDFESDTFFPIDLGKYLPEYGVLSVQSEKGIKYKPE 181
QY 181 VYEKND 186
DB 182 VYEKND 187
RESULT 11
Q86XF0 PRELIMINARY; PRT; 187 AA.
AC Q86XF0;
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DE 01-JUN-2003 (TReMBLrel. 24, Created)
DE 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein LOC200895.
GN Name=LOC200895;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
EX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045541; AAH45541.1; -.
DR HSSP; P00374; 1KNS.
DR GO; GO:0004146; F:dihydrofolate reductase activity; IEA.
DR GO; GO:0006545; P:glycine biosynthesis; IEA.
DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
DR InterPro; IPR001796; DHRP.
DR Pfam; PF00186; DHRF_1; 1.
DR PRINTS; PRO0070; DHRP.
KW Hypothetical protein.
SQ SEQUENCE 187 AA; 21620 MW; BA6548FB0F576FF7 CRC64;

Query Match 89.5%; Score 875; DB 2; Length 187;
Best Local Similarity 92.9%; Pred. No. 1.6e-69;
Matches 170; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 LNCIVASQNMIGKNGDLPMPFFLRNEFRYQRMVTTSSVEGKQNLVIMGKWTFSIPEK 63
DB 5 LNCIVASQNMIGKNGDLPMPFFLRNEFRYQRMVTTSSVEGKQNLVIMGKWTFSIPEK 64
QY 64 NRPLKGRNLVLSRELKEPPGGAHFLSRLDALKLTPQELANKVDMVIVGSSVYKE 123
DB 65 NRPLKDRNLVLSRELKEPPGGAHFLSRLDALKLTPQELANKVDMVIVGSSVYKE 124
QY 124 AMNHGHLKLVFTRIMQDFSDTFFPEIDLEKYLKLLPEYFGVLSDVQEGKIYKFEVYE 183
DB 125 AMNHGHLKLVFTRIMQDFSDTFFPEIDLEKYLKLLPEYFGVLSDVQEGKIYKFEVCE 184
QY 184 KND 186
DB 185 KDD 187

RESULT 13
AAH63379 PRELIMINARY; PRT; 187 AA.
AC AAH63379;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DE 02-NAR-2004 (TReMBLrel. 27, Last annotation update)
DE LOC200895 protein.

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OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fanev J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RA Submitted (DSC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063379; AA063379.1; -
SQ SEQUENCE 187 AA; 21634 MW; BA6548FB0F410327 CRC64;

Query Match 89.4%; Score 874; DB 2; Length 187;
Best Local Similarity 92.3%; Pred. No. 1.9e-69;
Matches 169; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 4 LNCIVAVSQNGIGKNGDLPWPFRLNRFYQFMRTTSSVEGKQNLVINGKKTWFSIPEK 63
DB |||||
QY 5 LNCIVAVSQNGIGKNGDLPWPFRLNRFYQFMRTTSSVEGKQNLVINGKKTWFSIPEK 64
DB |||||
QY 54 NRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTPQLANKVDWMIWVGSSVYKE 123
DB |||||
QY 65 NRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTPQLANKVDWMIWVGSSVYKE 124
DB |||||
QY 124 AMNHGHLKLVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVSDVQEEKGKIKYKEVYE 183
DB |||||
QY 125 AMNHGHLKLVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVSDVQEEKGKIKYKEVCE 184
DB |||||
QY 184 KND 186
DB |||
QY 185 KDD 187
DB |||

RESULT 14
DYN_PIG STANDARD; PRT; 186 AA.
AC P00377;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Dihydrofolate reductase (EC 1.5.1.3).
GN Name=DHFR;
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
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RX MEDLINE=80049777; PubMed=500653;
RA Smith S.L., Patrick P., Stone D., Phillips A.W., Burchall J.J.;
RT "Porcine liver dihydrofolate reductase. Purification, properties, and
RT amino acid sequence.";
RL J. Biol. Chem. 254:11475-11484(1979).
CC -1- CATALYTIC ACTIVITY: 5,6,7,8-tetrahydrofolate + NADP(+) = 7,8-
CC dihydrofolate + NADPH.
CC -1- PATHWAY: Essential step for de novo glycine and purine synthesis,
CC DNA precursor synthesis, and for the conversion of dUMP to dTMP.
CC -1- SIMILARITY: Belongs to the dihydrofolate reductase family.
DR PIR; A00389; RDGP.
DR HSSP; P00374; LKMS.
DR InterPro; IPR001796; DHFR.
DR Pfam; PF00186; Dihfolate_red; 1.
DR PROSITE; PR00070; DHFR.
DR PROSITE; PS00075; DHFR; 1.
KW Direct protein sequencing; NADP; One-carbon metabolism;
KW Oxidoreductase.
FT MOD_RES 162 162 Cysteine derivative (partial).
SQ SEQUENCE 186 AA; 21455 MW; D05DBS26FE5C12CE CRC64;

Query Match 88.1%; Score 862; DB 1; Length 186;
Best Local Similarity 88.2%; Pred. No. 2.2e-68;
Matches 164; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 VGLNCIVAVSQNGIGKNGDLPWPFRLNRFYQFMRTTSSVEGKQNLVINGKKTWFSI 60
DB |||||
QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTPQLANKVDWMIWVGSSV 120
DB |||||
QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTPQLANKVDWMIWVGSSV 120
DB |||||
QY 121 YKEAMNHGHLKLVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVSDVQEEKGKIKYKPE 180
DB |||||
QY 121 YKEAMNHGHLKLVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVSDVQEEKGKIKYKPE 180
DB |||||
QY 181 VYEKND 186
DB |||||
QY 181 VYEKNN 186
DB |||||

RESULT 15
DYN_BOVIN STANDARD; PRT; 186 AA.
AC P00376;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Dihydrofolate reductase (EC 1.5.1.3).
GN Name=DHFR;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=83000246; PubMed=7115669;
RA Lai P.-H., Pan Y.-C.E., Gleisner J.M., Peterson D.L., Williams K.R.,
RA Blakley R.L.;
RT "Structure of dihydrofolate reductase: primary sequence of the bovine
RT liver enzyme.";
RL Biochemistry 21:3284-3294(1982).
CC -1- CATALYTIC ACTIVITY: 5,6,7,8-tetrahydrofolate + NADP(+) = 7,8-
CC dihydrofolate + NADPH.
CC -1- PATHWAY: Essential step for de novo glycine and purine synthesis,
CC DNA precursor synthesis, and for the conversion of dUMP to dTMP.
CC -1- SIMILARITY: Belongs to the dihydrofolate reductase family.
DR PIR; A00388; RDBOD.
DR HSSP; P00374; LDHF.
DR InterPro; IPR001796; DHFR.
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pfam; PF00186; Dihyfolate_red; 1.
 PRINTS; PR00070; DHR.
 PROSITE; PS00075; DHR; 1.
 Direct protein sequencing; NADP; One-carbon metabolism;
 KW Oxidoreductase.
 SQ SEQUENCE 186 AA; 21472 MW; A615136C7706677F CRC64;
 Query Match 87.1%; Score 852; DB 1; Length 186;
 Best Local Similarity 86.0%; Pred. No. 1.7e-67;
 Matches 160; Conservative 13; Mismatches 13; Indels 0; Gaps 0;
 QY 1 VGLNCIVAVSQNMIGIKNGDLPWFFLNEFRYFQRMVTTSSVEGKQNLVIMGKKTWFSI 60
 DB 1 VRPLNCIVAVSQNMIGIKNGDLPWFFLNEFRYFQRMVTTSSVEGKQNLVIMGKKTWFSI 60
 QY 61 PEKNRPLKGRINLVLSRELKEPPGCAHFLSRSLDDALKTEQPELANKVDVWVIWVGSSV 120
 DB 61 PEKNRPLKGRINLVLSRELKEPPGCAHFLSRSLDDALKTEQPELANKVDVWVIWVGSSV 120
 QY 121 YKEAMNHGHLKLFVTRIMQDFESTPPPEIDLEKYKLLPEYPGVLSDVQEEKGIKYKPE 180
 DB 121 YKEAMNHGHLKLFVTRIMQDFESTPPPEIDLEKYKLLPEYPGVLSDVQEEKGIKYKPE 180
 QY 181 VYEKND 186
 DB 181 VYEKNN 186

Search completed: November 19, 2004, 13:49:40
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